

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGTGCCTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCCGCGCCGGAGGCCGCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAAACAGGGGATGGTGGACACCGCAAAGAAGAAGCTTTGGCGCGGGGAACA
CGGCTTTGGGAGGAAAAGACGCTGTCTCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCTGACTTATTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGGGTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCGTGAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAACGTCTACAATACTCCAGGGAGCTACGTCTGTGTGTCTCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGCGAAGACCTGTTAATGTGCGCGACTTACCCTTTAAATTATTTCAGAAGGATGTCC
CGTGAAAAATGTGCCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTTAAACAGCTGCATTCTCTGGTTGTTCTTA
AACAGACTTGATATATTTTGATACAGTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCAACTTGTTTATTGACGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACT
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTTGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAGTTAGGTGTGGAAAGTCCCGAGGCTCCCGCAGGCGAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

0360759-071001

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRRAALGLLPLLLLLPPAPEAAKKTPCHRCRGLVDKFNQGMVDTAKNFGGGNTAWEKILSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQKSEYPDLFEWFCVKTILKVCCSPGTYPDCLACQGGSQRPCSG
NGHCSDGSRQGDGSCRCHMGYQGFLCTDCMDGYFSSLRNETHSICTACDESKTCSGLTNRDCGEVGVWLDE
GACVDVDECAAEPSPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAECT
CVRKNENCYNTPGSYVCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCTCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACCGGAAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCTAGGTTGGC
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGAGCGCCTTC
CCTGCCGCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCTGTGGCACTGCGGGCGGAGGC
CGGGCCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTACCAGGCCAAGATACTCA
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGATACTTCTATGAATTCCTGTCTTGGCTCCCTGGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTCCCATGTCCTTGGAAAAACAGGATGGGGTGGCAGCATTGAACT
GGATGTGATTGTTATGAATTTCTGAAGGCAACACCATTTCTCCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAGCTGAGTGCCCGAGCGGGTGCCGAAATGGAGGCTTTTGTAAAT
GAAAGACGCATCTGCGAGTGTCTGTATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAATGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTCTACCCCTGGAAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCTGTGCAAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAAGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAAGAAGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCCCTTCACTTAAAAAGGCCGAGGAGCGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA
TGTGTTGAATGTTCAAATAATGTTTCATTACACTTAAGAATACTGGCCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCCTTTTAAAGTTTCTAAGTACGCTGTAG
CATGATGTTATAGATTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTCAAATTAACATGATTATGGT
GTCCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTTGGGCAAAAATGCGTAAGTCACAAGAA
TTGGATGTGTCAGTTAATGTTGAAGTTACAGCATTTTCAATTTTATTGTGATATTTAGAT
GTTTGTACATTTTAAAAATTTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC
TTACCATTATTTCCAGAGATTCAATATTAACCAAAATTAACACTGTGGTAGTGGCATT
AAACAATATATATATTCTAAACAAATGAATAGGGAATAATGTATGAACCTTTTGCAT
TGGCTTGAAGCAATATAATATATTGTAACAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAA
AAAAAAAAAAAAAAAAAGGGCGCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCATGGCCCACTGTTTATTGTCAGCTTATAATG

10012052200

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFFAAALWLSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGG
MAPPTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICIGSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

100120-6522060

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGGGGCCAGCCTGGG
CCCCAGCCACACCTTTCACAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCCGG
GAGCTAGCACCCGGGTCTGCACCTGCGGGGCATCCGGACGCGGGAGGCGCGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCCTCGGCGTGCCACCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCTGTATCTA
TCCAGTCTTGGGAAAGTACTGGGACAACCTGTAACCGTTGCACCTGCCAGGAGAAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTTCTGGGGCATGACCTGGATGAGGGGCATTGCTACCGCCTGGGCACCA
TCCGCCCATCTTCTCGGTGATGAACATGCATGAAATTTATACAGTGTGTAACCCAGGGGAG
GTGCTTCCACAGCCTTTCAGGGCCTCTGAGAAGTGGGCCAACCTGATTTCATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCCTGGGCCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCTGTCTGTGCGCCCGAGAACCCTGCTGTCTTGTGAC
ACCCACAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCTG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCCGACGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACCTCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGCGCATGGGACCCACTCAGTCAAGATCAAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCACATCGAG
AGCTTCGTCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCTACTGAGGCTG
CGGGCACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGCGGGAAGAGGCCCAATG
GGGCGGTGACCCACGCTCGCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGGCGCGGGTTCCGCTGACGACGCGCCCGCTGGGAGTCGCGGCAGGCAGAGCTGGCG
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCTGGCTCGGGAAGAGCACAGCTGCAG
ATCCAGGCCTCTGGGCGCCCCACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTAATCTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCAGGTTGAGATGCAGTGGGCCATCAGGGCTCACTGTAACCTCCGACTCTGGGTTCA
AGTGACCTCCCACTGACCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC
TAATTTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCCGAAC
CTGGGCTCAAGCGGTCCACTGCTCCGCTCCCAAAGTCTGGGATGTCAGGCATGAGGC
ACTGCACCCAGCCTGTATTCTTATCTTTCAGATATTTATTTTCTTTTCACGTGTTTAAAA
TAAACCAAGTATTGATAAAAAAAA

10012059.0.100

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPGLGLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

09902759.071001

FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTGCTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCCTGGTGGTTCTTGCCTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGCATGGGACCCACTCAG

0992759.071004

FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTCGCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCGCTGCAGCCCACTGGGTGTGGTGCCCGAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCAACCCTGTCCCCACCTGACCTCCCATGGCCCTCTCCAGGACTCCCAACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCTGCAGATGGCCCTCCAACCTCTCTGTGCTGTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

0906259.071001

FIGURE 9

MTHRTTTWARTSRAVTPTCATPAGPMPCSRLEPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMVCTPVPHDPMPALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPFAFSTLNPVLRHLFPQEAFFPAHPIYDLSQVWSVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

09602759.071001

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCAAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGGCCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAAACCTACAGCAGGACCAGTGGCAAGCA
CGTGCAAGTACCCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGAAGCCAGCGGGAAGACAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACTATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTCACGTAGTCTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCCGCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTGAGCGACTGAAGGCCTTGACAGACAACCGCTGAGGTGGCTGTCTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTTGTGTTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCTCACATTCCACGACCCAGGCCTGCACCCCACCCCCAACTCCAGCCC
CGGAATAAAACCATTTTCTCTGC

0906259.071001

FIGURE 11

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLIGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMFTRQGRPRQASRSRQNRQEAHFIRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

100170.652069

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTTCACATGGAG
GACAGACGCAAGAGGGCCACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTCTTTTCCACCACATTGTATTTTTAT
TTCGCTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCCT
GAAGTCTTGGCTTTATCATTTTCCCTGGGGCTCTACTCACAGGTGTCCAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGC
TGGATTTCTGCGAACTGCACAAATGTACAGTCCGGTGCACACGGTCTACCTGTATGGCAACC
AATGGACGAATTCCTCATGAACCTTCCCAAGAATGTGAGAGTTCTCCATTTCAGGAAAAAC
AATATTACAGACCATTTACCGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAATTTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTCCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTTGTACGTAATTCGCTGTCC
CACCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACAGAT
AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGTATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAAATGGCTCAA
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTTGAACAAGTCCGG
GGATGGCCGTGAGGGAATTAATATGAATCTTTGCTCTGCCACACGACCCCGGCCCTG
CCTCTCTTCAACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTCTAT
TCCAAACCTAGCAGAAGCTACAGCCTCCAACCTCTACCATCGAAACTTCCCACGATTC
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACTATTTCTGAACGGATCCAGCTCTCTATC
CATTTTGTGAATGATATCTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATA
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC
CACCAACCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCACAGCATGGGCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
GTGCTGGTGGTCTTGCTCAGCGTCTTTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGGCCGGCGGAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTAGATCTGCTCCTTTAAATACGAT
CAACTCCTTAAAGGAGATTTAGACTGCAGCCATTACACCCCAATGGGGCAGCTTAATTA
CACAGACTGCCATATCCCAACAACATGCGATATGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTCAGCAGCCAGAGGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGGTGTGTGCACATAAAGACACGCAGATTAATTTGATAAATGTTACACAGATGCAT
TTGTGCAATTTGAATATCTGTAAATTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACCTTTTGCTTTTAAATCTT

03902759-071001

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLVYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFPMNLKPNVRVLHLQENNIQTI
SRAALAQLLKEELHDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMAVRELNMMLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPITPDWDGGERVRTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWYKNGRRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

05932734-071001

FIGURE 14

ACTTTGGAGCAAGCGCGCGCGGAGACAGAGGCGAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCACGAGCGG
ATCCCCGAGGAGAGCCCGCGCCCTCGCGGAGGCGAAGAGGCGCAGAGGAAGACCCGGGTGGCTGCGGCCCTTGCC
TCGCTTCCAGGCGCGCGGGCTGCAGCCTTGCCCTCTTGCTCGCCTTGAATTTGAAAATGGAAGAGCTTCGCGAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCTCTCTCCCTGCGAGGCGCAGGGAGCGGTACGCTGGGAGGTCATCT
CTAGGGGCGAGACAGCTCGGAGCCACCCGAGACGGCCCTCTGGAGAGTTCTCTGGAGAAACAAGCGGGGAGAAC
TGGTTTTTCATCATTTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAAGGTCAAGGAGTTTCATCTGGTGACA
TCTTGCATTTCTTGGACATTTGGTCTGATGTCAACCCGAGTGGGCTGCTCCTCAATATGGCAGCACTGTCAAGAAATG
AGTTCTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTCTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCTTCAAGTATGCCCTGAACATCGCATTTCTCAAGAGGAGGGGGCCCGGCCCTTGA
GGGAGATTTGCGCAGGGCTCATTAATGATCTGTGACAGATGGGAGCACTCAGGAGTCTCCGTGGCGAGGTGGCTGTCTA
CTGACCGGAGACACGGGCTCTTAATCTTTGCCATTGGTGTGGGCGAGGTAGACTTTCAACACCTTGAAGTCCAGTTA
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAAATTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGCGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCATCTTCGCATCAACATCCCTG
GCTCATACGTCTGAGGTCGCAACAGGCTACATTTCTCAACTCGGATCAGACAGCTTGCAGAACTCAGGATCTGT
GTGCCATGAGGACCAAACTGTGAGCAGCTCTGTGTGAATGTGGCGGGCTCTTCGTCTGCCAGTCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTTGTGTGGCTGTGGACTACTGTGCCCTCAGAAAACACGAGTGTGAAC
ATGAGTGTGTAATGTCTGATGGCTCTTACCTTTGGCAGTGCCATGAAGATTTGCTCTTAAACCCAGATGAAAAAA
CGTGACCAAGGATCAACTACTCTGTGCACTGAACAAACCGGCTGTGAGCATGAGTGGCTCAACATGGAGGAGAGCT
ACTACTGCGCTGCCACCGTGGCTACACTGTGAGCCCACTGCAAGGAGGCTGACAGGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGTGAGAAGGCTTCC
TCATCAACGAGGACCTCAAGAGCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTGTGGAATACCTCT
GTGTCAACATGAGCAGATCCTTTGCTGTGTCAGTGTCTCGAGGGACACGCTGCTCGCAGCGATGGGAAGACGTTGT
CAAAATTTGGACTCTTGTGCTCTGGGGGACACCGGTTGTGAACATTCGTGTGTAAAGCAGTGAAGATTCGTTTGTGT
GCCAGTGCCTTTGAAGGTTATATACTCGTGAAGATGGA AAAAACCCTGAGAAGGAAGATGTCTCGCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGGTGCTTGGAGGGATTCGCGCTCG
CTGAGGATGGGAACGCTGCGGAAGGAAGGATGTCTGCAAAATCAACCCACATGGCTGGCAACCATTTGTGTGA
ATAATGGGAATTTCTATCATCTGCAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAGAAAT
GCACTGAAGGCCCAATGATGCTTGTGTGATCGATGGATCCAAAGAGTCTGAGGAAGAGAGATTTTGAAGTCTG
TGAAGCAGTTTGTCACTGGAATTTATAGATTCCTTGACAAATTTCCCCCAAGCCGCTCGAGTGGGCTGTCTCAGT
ATTTCCACACAGGTCCACACAGAGTTCATCTGAGAAAATTCAACTCAGCCAGCAAGACATGAAAAAGCCGTGGCCCC
ACATGAAATACATGGGAAAGGGCTCTATGACTGGCTGGCCCTGAAAACATATGTTGAGAGAAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCTTTTCCACAAGGGTGCCAGAGCAGCCATTTGTGTTCCAGACGGAAGCGGCTCAGGATG
ACGTCTCCGAGTGGGCGAGTAAAGCCAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATG
AGGAGGAACTACAAGAGATTGCTCTGAGGCCACAAACAAGCATCTCTCTATGCGCAAGACTTCAGCACAATGG
ATGAGATAAGTGA AAAACTCAAGAAAGGCATCTGTGAGGCTTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACTGCCAAAACCGTCCAAACAGCCAAAGAAATCTGAGCCAGTACCATAAATCTTCAAGACCTACTTT
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTTACACAAAAGCTTT
TCCAGAACCTTGCAACGAAGAAGTAAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAATAATCGCTGAGATACAGATGAAGATTAAGAAATCGCGACACATTTGTAGTCAATTTGATCAGCGATTACAAT
GAAACGAGTGCAGAGGCCCAAGGCTCAGGCTATTTGTTAAATCAATAATGTTGTGAAGTAAAAATCAGTACTGA
GAACTCTGTTTGGCCACGAAACAAAGACAAAGATATACACTAATTTGATATAAATTTATCTAGGAAAAAATCCCT
TCAGAAATCTAAGATGAATTTACAGAGTGAGAATGAATAAGCTATGCAAGGTATTTTGAATATATCTGTGGACAC
AATCTGCTTCTGCTTCTGCTTCTAGTGTGCAATCTCAATTTGACTATACGATAAGATTTGCAACAGTCTTACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGTGACCTTACCTTGATATATGTATATGGATGTATG
CATAAAATCATAGACATATGTACTGTGTGAACAAGTTGGATTTTTATACAAATATAAAATTCACCACTTCAG

100170-0-6520360

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCAGCTCCGGCCGTGCGCAGCCTCG
GCACCTGCAGGTCCTGCGTCCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCAGCGTGGTACACCTTGACACGGGAGGTGTCTTC
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTCATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGAAGACAAACAAGGCAAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCCGTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGACCCCTGCCTGGCCCAAGAGCTCAGACACAATGTCCAAGAATGGGACCCT
TTCCTCTGTCACTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCA
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTAT**TGA**TGAC
CCCACCACTCATTTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCCACCCCTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTGTTTTTCATTGCAAAATTTAAATAAGATACATAA
TGTTTGTATGAAAAA

0302759-071001

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLFANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVFPVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNLVLPAPPSCRLQGVPHVGANVTLSQCQSPRSKPAVQYQ
WDRQLPSFQTFPAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGP RP PGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

100120-0520660

FIGURE 18

CGCCACCCTGCGGCCACCGCCAATGAAACGCTCCCGCTCCTAGTGGTTTTTCCACTTTG
TTGAATTGTTCTCTATCTCAAAATGACCAAGACACCTTGCTCTCCCAATGCAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGCACAA
TTTTGTGAAGATGATAATGAAATGTGGAAATTTAACTCAGTCTGTGGCGCAAAATGCTAAATGTC
ACTAACACAGAAAGGAAGTTATTTATGTTATGTTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTTATCATTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT
TAGATAATGTCGTATAGCTGCAAAATATTAATAAACTTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTTTGCTACAGAAAGTCTATAGAAAATTTCTGTGACAGATCTTTTCAACCAACAGA
TATAAATACATATATAGAAATATAGCTGAATCATCTTATTACTAGTGTACAAGAACCAACA
CTATCTCAGCCAAGGACACCTTTCTAACTCAACTCTTACTGAATTTGTA AAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAATTCACCGGATATAGCTCTCAAAGTTTTCTTTTTGTAT
TCATATAACATGAAACATATTTCATCCTCATATGGAATGGATGGAGACTACATAAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATA
AGAGTATTGGTCCTTTGCTTTTCATCATCTGACAACTCTTATTGAAAACCTCAAAATTTATGAT
AATTTCTGAAGAGGAGGAAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACCTGAAAAAATAACATTACATTAAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTTTGAATTTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGCTGTGAGCTGACATACCTCAAATGAGACCCACCTCATGCGCTGTGAATCACCT
GACACAGTTTGAATTTTGATGTCTCTGGTCTCTCCATTGGTATTAAGATTATAATATTC
TTACAAGGATCACTCAACTGAGGAATAATTATTTCAGTGAATTTGCTTGGCATATGCATTTTT
ACCTTCTGGTTCTTCAGTGAATTTCAAAGCACCAGGACAACAATTACAAAAATCTTTGCTG
TAGCTATTTCTTGCTGAACCTGTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTTGCCGACTGCTACACTACTCTTTTTCAGTCTGTTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTTGTTGGGTGTCATCTACAACAGGGATTTTGTGA
CAAGAATTTTTATATCTTTGGCTATCTAAGCCGAGCGTGGTAGTTGGATTTTTCGCGAGCAC
TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAAAACAATTTTATT
TGGAGTTTTATAGGACAGCATGCCTAATCATCTCTGTTAATCTCTTGGCTTTTGGAGTCAT
CATATACAAGATTTTTTCGTCACACTGCAGGGTTGAAACAGAAAGTTAGTTGCTTTGAGAAC
TAAGTCTGTGCAAGAGGAGCCCTCGCTCTTCTGTCTCTCTCGGCACCACCTGGATCTTT
GGGTTCTCCATGTTGTGCAGCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGC
TTTTCCAGGGGATGTTCAATTTTTTATTTCTGTGTGTTTTATCTAGAAAGATTCAAGAGAAT
ATTACAGATTTGCAAAATGTCCTCCCTGTTGTTTGGATGTTTAAAGGTAAACATAGAGAAAG
GTGGATATTGATCAACTGCAAAAAATAAAAAATCCAAAGCTGTGGATGACCAATGTTATAAAA
TGACTCATCAAATATCCAATTATTAACACTAGACAAAAAGTATTTTAAATCAGTTTTTCT
GTTTATGCTATAGGAACCTGTAGATAATAAGGTAATAATATGATATCATATAGATATACATATG
TTTTCTATGTTGAATAGTTCTGTCAAAAATAGTATTGCAGATATTGGAAGTAAATTTGGTT
CTCAGGAGTGATATCACTGCACCAAGGAAAGATTTTCTTCTTAACACGAGAAGTATATGAA
TGTCTGTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTCCTTTGAAACTAGTCC
CTACCACTCCGTAAATGAGCTCCATTACAGAAAGTGAACATAGAGAATGAAGGGGCGAGA
ATATCAAAACAGTGAAGAGGAATGATAAGATGATTTTGAATCAACTGTTTTTTCTGTAGAC
TAGCTGAGAAATTTGTTGACATAAAATAAAGAAATGAAGAAACACATTTTACCATTTTGTGAA
TTGTTCTGAACTTAAATGTCCACTAAAAACAATTAGACTTCTGTTTGTCTAAATCTGTTTCTT
TTTCTAATATCTAAAAAAGAGGTTTACCTTCCACAAATTTGAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAA

CGCGCTG-071001

FIGURE 19

MKRLPLLVVVSTLLNCSYTONCTKTPCLPNAKCEIRNGIBACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLNDVNCIAA
NINKTTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYIEILAESSSLGYKNNTISAKDTL
SNSSTLTLEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKFVFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAFAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEEERVISVSVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPTDMNGSWSSEGCETYSNETHTSCRCNHLTHFAILMSSGSPSIGIKDYNILTRITQLG
IIISLILCLAICITFTFWFFSEIQSTRTTIHKNLCCSLFLAELVPLVGINTNTNKLFCSTIAGL
LHYFFLAAPAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFIIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVHVHASVVTAYLFTVSNAPQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAAC TTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATT TTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTGTCTTGCCATATGCATTTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

100120-6522060

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGGCTCCTCCTCCCGCAGATCCGAACCGCCTGGGCGGGGTACCCCGGCTGGGA
CAAGAAGCCGCGCCTGCTGCCCGGGCCCGGGGAGGGGCTGGGGCTGGGCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTATATATAAGGCTGCCGGCCCGGAG
CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCGCAACCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGTGGAAGTGGCGCGGGGGC
CAGAGCGCGCACAGTTTGTGGAGATCAAGGCAGTCTGCTGCGGACCGTGGCCATCAAGGG
CGTGCAAGCGTGGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTAACGA
TCCGAGAAGCACCGCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTCTGCCCCATGCTGCCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGGAACTCTGACATGTTCTCTGCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTACCCGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAAGT
GAGACCATGCCCCGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCTGAGTCCACGTCTGTCTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAGAGTTTTCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCTGGGCCCCCATCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCTTTGGAAAAATCTTATGTCAAGCTGAAATTCCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTAAATTCAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTTCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCCACG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGCAACTTGAGAATTCCTC
CTGAGGCCAGTTCTGTCATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGTC
TTCATCTCCCAGCCCCAGCCCTCTGCCACCTCACATGCTCCCATGGATTGGGGCCT
CCCAGGCCCCCCACCTTATGTCAACCTGCACCTTCTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCGCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGTATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCCAAAATATATTTATGTATGTAGTGAGGTTTG
TTTTGTATATTAAATGGAGTTTGTTTGT

FIGURE 22

MRSGCVVHVHVLWILAGLWLA VAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALTVAIKGVHSVRYLCMGADCKMQQLLQYSEEDCAFE
EIRPDGYNVYRSEKHLRPFVSLSSAKQRLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

0990759-021001

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCTCTGCGCTCTGCGCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCGCCCCCGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAAACTGGGTCGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTGTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAACAATGAATACAAAACCTGGAAC
TGCATTTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCGTGAATCCAGCACTTTGGAAGG
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAAATAAATAAATAAATA
AATAAATACTGGTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

0902759-071004

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSVFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQQLNEED
TVTLEVLVAPAVPSCFVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

100120-652066

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTATTATTAACATGCTCCACAGCCCGGACCCCTGGGCAT
CATGCTGCTATTCTCGCAATACTGAAGAAGCATGGGATTATAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTTCTCTCTCCAATATGCATGACATTTTGGACAATG
CAATTGTGGCACTGGCATTATTTCAGTGAAGAAAACTTGTGTTCTTATGGCATTTCATCA
TTTGACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAATCCTTAAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCCTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACCTCCAGAG
ACTTTCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTACCACAT
ATTAATGTAAAAAAGATGCCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACCTTACTGA
ACTGCCTGAAAAATGTCTGTGCCAACTGAGCAACTTACAAGAACTCTATATTAAATCACAAC
TGCTTTCTACAATTTCACTGGAGCCTTTATTGGCCTACATAATCTTCTCCAGCTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGTATGCTCTTCCAATCTAGAGAT
TCTGATGATTGGGAAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAAGCCTCTTATCA
ATCTTCGCGACCTGGTTATAGCTGGTATAAACTCACAGAAATACCAGATAACGCCTTGGTT
GGACTGGAACCTTAGAAAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAACTCCTATTAAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAAATATGCCT
GAGCTGATTTCCATCGATAGTCTTGTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTCACCCCAATGCATTTTTCAGACTCCCCAAGCTGG
AATCACTCATGTGGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG
GATGAACATGAACAAACCAACATTTCGATTTCATGGAGCCAGGATTCATGTTTTGCGTGGACC
CACCTGAATTCAGGTCAGAATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCCTTTCAGTGTAGAGCTACTGCAGAACCCAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTCTGCCTAATACCTGCAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAAATGGCGTAACCTCCAAAGAAGGGGTTTATATACTTGTATAGCACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTCCACAAGATAACAATG
GCTCTTTGAATTAATAAATAAGAGATATTCAGGCCAATTCAGTTTGTGGTGTCTGGAAAGCA
AGTTCTAAAATTTCTAAATCTAGTGTAAATGGACAGCCTTTGTCAAGATCAAAAATTTCTCA
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAAATTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAATGTGCACCAACCAAGGTTTGCACCTGTATCAAAAAGAGTATGAAAGAAATAAATC
CAACAACCTTATGGCCTGTCTTGGAGGCCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAAGTGAAGTGTGATGTTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTGTGATAAATCTCTGGGAAGCAGGAAA
AGAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACACCAAGGAAACCTACTCCAAAAATGAAC

09902759.071001

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGA AACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAACGTCCTGTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGTTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTTGCATTTGCAGTAGAAAATAAGTGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCAGTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAAGCTTAACTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

09902759-071003

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTC SNANLKEIPRDL
PPETVLLYLD SNQITSIPNEIFKDLHLRLVNL SKNGIEFIDEHAFKGVAETLQTLDSL DNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVI CKTSVLDEHAGRPF L
NAANDADLCNL PKKTTDYAMLVTMFGWFTMVISYVVVVYVRQNQEDARRHLEYLKS LPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

0360759-07100
000720-0520360

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCTGCTGGCAGCCCATCTCTGCTGGTGTCT
GGGCTCAGTGCTGTGAGGCTCGGCCACGGGCTGCCCGCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCGAGGGCATCCCCACCGAG
ACGCGCCTGTGAGCTAGGCAAGAACCAGCATCAAACCGCTCAACCAGGACGAGTTCCGCCAG
CTTCCCGCACTGGAGGAGCTGGAGCTCAACGAGAACTCGTGAGCGCGCTGGAGCCCGCGG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCTTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGACACCATGACACCCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCGCCCACTAGTCTATCTCCGCTTCTCTCAACCTCTCTTACAACCCCATCA
GCACATTGAGGGCTCCATGTTGTCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCACTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCCTCAACTACCTGCGCGTGTCTAA
TGTCTCTGGCAACAGCTGACCACACTGGAGGAATCAGTCTTCACTCGGTGGGCAACCTGG
AGACACTATCCTGGACTCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACCGCCAGATTGTCCA
GGGCAAGGAGTTCAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACTGCCCGCGG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGTGACGAGGGCCACACGGTGCAGTTT
GTGTGCCGGGCGATGGCAGCCCGCCGCCCATCTCTGGCTCTCACCCGAAAGCACTT
GGTCTCAGGCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCAGCTGGAGTGCCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACCGGGCGGCAACGAC
TCCATGCCCGCCCACTGCATGTGCGCAGCTACTCGCCGACTGGCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCCAACCAAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCACTG
TGCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCTGCTCCTCTTCTGCCTGGTGTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCAACATCGAGATCGAGTATGTGCCCCGAAAGTCGAGCAGGCATCAGCTCTCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATA**TG**AGCGCCGGGGCGGGGGGACGGGACCCCCG
GGCGCGCGGCGAGGGGAAGGGGCTGGTCCGCACTGCTCACTCTCCAGTCTTCCCACTCT
CTCCCTACCTTCTACACAGTTCTCTTCTTCTCCCTCCCGCTCCGTCCCTGCTGCCCGCG
CCAGCCTCTCACCACCTGCCCTCTTCTACCAGGACCTCAGAAGCCCAAGACCTGGGGACCCCA
CCTACACAGGGCATTTGACAGCTGGAGTTGAAAGCCGACGAACCCGACCGCGGAGAGTCA
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTTGGGTTTCAATAATTATGGAATTT
TATGAAAACTTGAATAATAAAAAAGAAAAAACTAAAAA

0906259-071001

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASPPHLEELNENIVSAVEPGAFFNNLFNRLTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLSLEQLTLEKCNLTSTIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPLYDTMTFNCLYGLNLTSLSTHNCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMLEHL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNETLIILDSNPLA
CDCRLLWVFRRRWRLNFNRRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGPPPAIWLSPRKHLVSAKSNGRILTVPFDGTLEVRYAQVDNGTYL
CIAANAGGNDSPAHLHVRYSYSPDWPHQPNKTFAFISNQPEGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGN TKHNI EIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCTCCCATCCCCAGCCCCGGGATTTCAGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCCGGAAGCGCGATCGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC
TGTTTCGCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCTAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTTCAGCTGGTTACCTCTACGCCCCAGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCATATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCTAAACTGTGAGTCTTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTGTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGCCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCACTTCTGTC
GCCCCCAGGGGCCCTGTGGGGACTGTGGGGCCGTACCAACCCGACTTGTACAGAGCAA
CCGAGGGCCGCCCTCCCGCTTGTCTCCCAGCCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGAATGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCCTGGCTTCTCTGCATTGCGGTTATTATTATTTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAAGCAAAAAACA
AACAAAAACA

09962759.071001

FIGURE 32

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRILQVLTSTPHELISISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHCEGRGNFVPQQYLWEKEGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGYLTAEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

100120-623494

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCACCACCCCAAAACCTTTTCTTCTCCTTTCTCTGG
CTTCGGCAGATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGAGCGTCTCTTTGTTTTCGCCGTGGAACGTTACAGGGGACGTTTGCAAAAGAGAAGA
TCTGTTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCCCGGACTTCCAGTTTACCATTATTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTCTGGGGCTGCAGCTGGTGAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAATCCCCTGGTATTGCGGAGATCTGTCTAGAGGATAACCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGAAAAACATTCCCAAGAATGCC
CTGATCGGCCGAGTGTGCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAAACAGGACTTGTGCTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCGCAAG
GATCATGCCACACCGAGGTCTGCTCCAACCGGAGGTACAAAGATCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCATAGCGAGCGGTAGCTCCAGGAACAAACCTTAGCTAACA
GTTTACCCTGCCCTGGGGCTGCGAGCTGCGACCATCCAGGGTCCGGTTTAAAGATGAAC
TGCAACACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTTCTGTGGATCTGGGCAACAATAACATCGTACTGTAGAGAACAAACACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTAACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCTCTCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCTGCTGGACGTGTTTCGCTGGGCTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCACTTAACCTCCATCATCCAGA
TAGACCTCCACGGAACCCCTGGGAGTGTCTCTGCACAAATTGTGCGCTTTCAAGACTGGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGCGCCGCTGAACTCTT
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACTCC
AACTCCTACCTAGACACAGCAGGGGTGCCATCTCGGTGTGGTCCCGGGACTGCTGCTGGT
GTTTGTACCTCCGCTTACCGTGGTGGGCTAGTCTGCTGTTTATCTCTGAGGAACCGAAAGC
GGTCCGAAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
TGCTCTCACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCTTCCCCACCGAGGCCACCCCGGGGCTGGAGGGGCTGTACCCTTCCCGGCT
CCATCAGCCTGGATGGGCATAGTAGATAAATAACTGTGAGCTCGCACAAACCGAAAGGGCCT
GACCCCTTACTTAGTCTCCTCTTGTAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGTGTAGAGCCCTTTTGACAGAAAGCCCGACACGCTGACCTTGAAG
AATGACAGTGCCTTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATATATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCTGTTGGCTACGCAGGGATGGGCACTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLPNEFANFYNAVSLHMENGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLVLILNDNLISTLPANVFQYVPI THLDLRG
NRLKTLPIYEEVLEQIPGIAEILLLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSLPAPPAQEETFAPGPLEPTPFKTNQGEDHATPGSAPNGGTK
IPGNWQIKIRPTAAAIATGSSRNKPLANSPLCPGGCSCDHI PGSGLKMNCNNRVSSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRLWLYMDSNY
LDTLSREKFAQLONLEYLNVEYNAIQILIPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSTIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPOLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTSFTVVGMLVFI LRNRKRSKRRDANSSASEINSLQTVCDDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGCGCCAGCTGTGTTCTGTACCCAGAACTCAGGGC
TGCACCGGGCTTGGCAGCGCTCCGCACACATTTCCTGTGCGCGCCCTAAGGGAACTGTTGGC
CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGTCCGTCGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGGCTCAG
AGAAATGAGGCCGGCGTTTCGCCCTGTGCCCTCCTCTGGCAGGCGCTCTGGCCCGGGCCGGGCGG
CGGCGAAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCTGTGTACAGCCTGC
ACCACGCTACCATTGAAGCGGCAGGCGGCCGAGGAGGCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG
GCCCGGAGGGGGCTCCAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCTCACT
GCACCTGGAGAACGAGCCTTTGCGGGGTTTCCTCTGGCTGTCTCCGACCCCGGGCGGTCTC
GAAAGCGACACGCTGCACTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGAGATGCGC
GGTACTCCAGGCCACCGTGGGGTCGAGCCCCGAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTTGCGCGCGCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGGACAACTCTCGGGCGATGTGTGTGTCTCCGCGCCG
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTTGCGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGCGCGCTCTGTGTGACCA
GTGGGGAAGGACAGCCGACCTTTGGGGGACCGGGGTGCCACACAGGCGCCGCGGCCACT
GCAACAGCCCCGTGCGCGAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTGAGTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCAGATGTCTACCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGAGCGTGATTTCAGGTTTAATTCTACGACTTCCTCTGCCACTCTCTCAGGCTTT
CGACTCCTCCTGTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACGACTTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCGCGGCTGGAGAGTGATCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCCTTGCTGGCGGAGTCCCCCTTTGGCTCTAGTGATGCATAGGGAAACAGGGGA
CATGGGCACCTCTGTGAACAGTTTTCACCTTTGTATGAAACGGGGAACCAAGAGGAACCTTAC
TTGTGTAACGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCCTGATGATAGAGGAAGTGAAGTGCCCTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTTCGGAGAA
TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAACAAATAGAACACAATATATTTTACA
TTAAAAAATAATTTTACCAAATGGAAGGAAATGTTCTATGTGTTGTTGAGCTAGGAGTAT
ATTGGTTCGAAATCCCAGGGAAAAAATAAAAAATAAAATTAAGGATTGTTGAT

100120.652000

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNL SYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGD CDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

100120-652060

FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGGGTATC
CCCCGGCTACCTGGGCCGCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGCTACAGCTGCC**ATGA**
GGGGCGCGAACGCTGGGCCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTCACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTAAGGTTTTCTGGAGTGTACCTCCAAATAGCAAATGTACTTGGAAAAATCA
CAGTTCGCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTACATAGACGCTCGAGAGTGACAA
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACITTCGGCGCTGGAGCCCTTGTGTCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCGGCTCTTTTAAAAAC
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTTGGTCACTACATATTCAGGCCAAAA
AAACTGCCCTACAACCTACAGAACAGCCTGTCAACCACCAATTCCCTGTAACCAACGGGTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTATCACAACCATCACTCGCGATGGGAGTTTG
CAGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACAGCAGCGCGG
CAAGAACATGAGTGCCAGGCTGACTGTGCTGCAAGCAGTGCCTCTCTCAGAAAGAGGTG
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCTTGATGCTTTAAAAAATAAGCAATG
TTAA**C**AGTGAACTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAACTTCTT
TGCTGCTGTCTCAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGCTTTATTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCATATTTATAGT
GTTATTGTCTTCACTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAA

03902759-071001

FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFCTCGGILTGESGFISGEFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTFFPVTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

0902759-071001
100120-652060

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGGGCTGGGGCGGTTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCGCTCAGCCCCATCCGTGTCTATACCTG
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAATAACAAGACAGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGTCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCCCTCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGTTATGTTCTGGCTGT
TTTGGCCCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCTTAGGCTGCATGGGGGCAGGGCCAGGTCGCTGTAAGAAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCGGGAGAGA
ACAAGCAGTGTGAAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCTAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCC
TCCTGTCTGGACACTCAGGACAGCTTGGTTTATTTTGTAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACTGGCGGGGACTGTCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCTGCCAGCTGCATGCTGCCAGTTCCCTGT
TCTGTGTTCAACCATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAA

090259.071001

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPQSSPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG
YGGAEACGQCGLGYFEARNASHLVCSACFGPCARCSGPRESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSEYECRDCAKACLCGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLLQQMFFG
IIICALATLAAKDDLFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

10070-6520660
9902759-071001

FIGURE 41

TGAGACCCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACCTCTGGGTGTTGCCCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCA'TCCCCACCCACGTGAGGGCCCCAGT
ACGTGGCCCTGTGTCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTT'GAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGT'TCGG
CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
AGCCGGT'CCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGGCTCCGCGACGACGGCTCCAAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCC'TTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCCGGCAGCCGCTGCTGTACTAGGTGT'CGGTGCAGAGG
GAGCATCTGGGCCCCGTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTTGAAGCACC'AATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCGAGGTGGTCAGCTGCCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCA'TAGCGCCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGT'TTTCTGAAGTGTTCGAGGTTACCAGGAGAGCTG
GCGATGACTGAAC'TGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAGTTACCTCACCTAATTTT'TGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACATATATTCTAAGCACTTACAT
GTGGAGATACTGTAACTGAGGGCAGAAAGCCANTGTGTCA'TTGT'TTACTTGTCTGTCCAC
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT
AAAA

0302759-071001

FIGURE 42

MQPLWLCWALWVLPASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVS VHESGWKA FDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGF LAYECVGTCTCRQPPEALAFKWP
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVS LPMNRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTCACTGGCCTGATCGCGAATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGCTCTGTGCCTACTCGGGCTTTTCTTCTCCCGTGTTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTT
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCCCTGTGACGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTTCATCGTGGCAGCCGTCTTGTAAACCTGATTCTCCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTCTGGTGTTGAGCCCTGGTCGGCTCACCGCCTATCATCTGCATTGCTTACT
CAGGTGCTACCGGACTCTGGCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTGAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTACCACTGCTGAGTGGCCTGGAACCTGTTTAAA
GTGTTTATTCCCCATTCTTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTCTGGGCTCTTCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCACTCTCTTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAAGCTTGAAGCCAAAAG
GATTTAAACCGCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

100125.0101

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSA YSGFSSPRVEW
KFDQGDTRRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAPFNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

100740.626069

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTGGATGGCGCAGGTGGAG
GCGTGGCGAAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCCGAGGCCCCAGCTCAG
GCTCGTGCCCAACCCACCAAGTTCCAGTGCCGCACCCAGTGGCTTATGCGTGCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCCTGACCCGGCGTCA
GTGACTGCTCTGGGGGAAC TGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCAGTGCGCTGCGACGGCCA
CCCAGACTGTCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCACTGTGAAGCCCCAACTGCCTATGGGGTTATTGAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCCTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGTGCCCTTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGCCCTGGAGATTGAGGGTCCC
TGGAACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAAGTGA
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 45

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDCSDGSDDEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGELRCTLSDDCIPLTWRC DGH PDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTS LR NATTMGPPVTLESVFSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLV TATLL
LLSWLRAQERLRPLG LLVAMKESLLLSEQKTS LP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

100120-522060

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCTATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGCATTTCCGAGAATGGCTTCAGGACCCACAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAAATGGAACCTAGGCTGGATCCCAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCTATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGTCTACAAAACCTTATCTGGTCGTCCAGCCACCCCGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTGCTCT
GCCACCCGCGGCCCTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACACGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCTTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCTCCTGA
CCAGTGGAAGATTGTGGCGTTCACGGCAACAGTGTGCTGCTGGTGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
TTCCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCCTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACCAAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGTCTCCAAA
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCTTGCTTCGGACAACCTTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCCCTGGGT
GTTGTTCTAAGAAATGGAATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTTCTTCTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAGNAAAAA

100140" 652466

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHPNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCRLRPLAS
SNGYVNISELQTSFPVGTVISYRCFFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDVFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPSPRSSSDPDFVVD
GVPVMLPSYDEAVSGGLSALGPYMASVGQCPLVDDQSPPAYPGSGDITDTPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

100120.522080

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCCGCTCCCGTGCGGTCCGTGCGCTTAGAGA
TGCTGCTGCGCGGGTTGCAGTTGTGCGGCACGCCTCTGCCGCCAGCCCGCTCCACCGCGGT
AGCGCCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGATGGAGGCCAGTCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
AAGTTTATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGAAGTATGGCAGCATAT
CACAATTTAGGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CCGGTGCAACATGAAGAACATTTTCAATTTGCAATATTTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCAGCATTCCCCTTCTCCTCCTCCTTGTTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAAACA
AAGCGAAGCTGACTTAGCTGAGACCGGCCAGACCTGAAGAATATTTTATTCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA
GTTCTCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAGTGAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAGAAATGATAAGCAAAATC
CTCTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCAGACCTCCTGTTGGACCCACGTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACACCTCTGTTTTCTTGCTCTATACAG
CAGCATATTTATCATACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

100120° 65220660

090255-021001

Signal sequence:

Transmembrane domain:

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCTCTCTGCAGCCTCAACCCGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCCGAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCGAGCTATTAGAGGTCCACCCCAAATC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGTGGGCAT
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCTTTTC
TTTACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAGCTGTCTGGAGCCCTGA
GGCAGAGAACCAGAGGCCGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTAATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCTGGGGATTTTGGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGTCTA
TTACCACGGGAAGGAGCAGGTCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAAATGCCATGTCACTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAGCAGGATGTGTTGATT
TTAAATAAAGTGCCCTTTATACAATG

100720.6520000

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLCLKMKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFAINGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTASLQPGISED LKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMTLGI FDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCLPDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

1001201520660

FIGURE 53

CTCCTCTTAACATACTTGACGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTACAGCTCATCACCTTACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCCTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCAGAGGGGTGT CAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAAACCATCTGGCTGAGCCAGATGT CATGCTCAGGACGAGAAGCAACCCCTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCTG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA
CCAGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTCTGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGT CATCTGCTCAGTGTAGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACATACATCA
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTTGTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

100760.6522066

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESSFSVPVEGVRLADGPGHCKGRVEVKHQNQWYTVTCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVVLHKGWGSVCDNNGEKEQVVKQQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

100170-5220560

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCTGCCCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGAA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCCAGTTGCTCTAACGAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCCGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG
AAAGACTGAAGAAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACT
AAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAGGGCGGCCGCACTTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCCACTTGTATTATGCAGCTTATAATGGTTAC

0362755.07301

FIGURE 56

MDFITSTAILPLLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLGCRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGMISI
PFRSAYAASKHATQAFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

100720-6528693

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAAATCAGTCACCGCGGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGTCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTCTTCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTGCTGTTGGGA
TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAAACACATG
TCTGTGTCCTAATTTTCGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAAACACATTGGAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAGGCACCTAGTTTTCTGAAAACGTATTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTAATGTTTGAACCTTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTGGAGGCTTGGCAGTCTTCATTACTACCCTTGTCTTTAGCCAAAAGCTGATT
ACATATGATATAAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACCTTAAATTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAAACITCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACAGTGTGCAAGTATAAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

100720-6520650

FIGURE 58

MKFLDDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDDAVIGYKMQA

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

100120-652053

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGCAACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCGCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTCTGGTTC
TTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCCTTATGTTGTCAACAAGTAACATGA
CCTTGGCTGACAGAGACTTCCCTTGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCCTAATTCAAGTTTTCCAGATATTTCCCTGAATATAAAAAATA
ATGACTTTTTATGTCACTGGGGAGTCTTATGCAGGGAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCTCAACCCGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGGAGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACCTATAGTTGAAAAAGTACTTGGCAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAGGATCCCGGAATACAAGAAGGCAGAAAAAAGTTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTTC
GAGGTGGAGGACATATTTTACCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTATGGAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCAAAAAGAGAACAT
CAGAGGTTTTATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAAATATCCTTGAACAAGTGAGC
TTTTGTTTTTGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGCTCTTGAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAAAGTGCAAGTTG
TAACAAACAAAGCTGTAACATCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCCAATAAATGGATGAAGCTATAA
TAGTTTTTGGGGAAGAAATTCCTCAATGTATAAAGTCTTAGAACAAAAAGAAATCTTTGAAATA
AAAAATATTATATATAAAGTAAAAAATAA

1001020259-071001

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGD SGQPLFLTPYIEAGKI QKGRELSL
VGPFVPLNMKSYAGFLTVNKTYSNLFWFPPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTLTSMLYIDNPFVGTGFSFTDDTHGYAVNEDDVARDLYSALI QF
FQIFPEYKNNDYFVTGESYAGKYVPAIAHLIHS LNPNVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNV TG
CSNYYNFLRCTEPEDQLYYVKFSLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
BIMNNYKVLIIYNGQLDIIVAALTERSLMGMDWKGSQBYKKA EKKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

100120.652060

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT
TTTTCCCTTTCTTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTCTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACCAAGCTTTCAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTTCAACAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAAGGGCCAGAAA
TAGAGATGCTTTGTAAAATAAAATTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCCTGGGT
AGGCCAGCCTCTTTGCTCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACAGAGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAAACAGAGGAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCGCTCTGTGGTCTCGTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCCTCAGTTCAGCACCTTCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
CCACCAAGGAGCGGGGCCGTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCCCTCACCAACAATGTCAACAAGCTGCT
CATCATGTACTACTGTAGAACCCTGCTGGCCTGTGGGAGCCTTACCAGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTTTCATCCTGGTGGAGCCATCCCAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCAGCCCTGTCCA
GCCGGAAGCTGCCCGGAGACCTTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCCTTTGACAT
CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCTGAGGGTGTGGCCATCACTCCGCTGGAGACCTCTCTACACCTCAGGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCACCTCATACGTGTCCTTGGCCCTTGGCTGCACCCGGG
CGGGGTGGAATACCGCCTCTGCAAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACCAAGCAGGACGATGTACTCTTTGCCATCTTCCAAAGGGCAGAAG
CAGTATCACCAACCGCCCGATGACTCTGCCTGTGTGCCCTTCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAAGACGTCCAGTGACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAAGCCTGGGAGGCTCAACTCAGTGGAGGGCTGACCTGTACACAC
CAGCAGGAGCCGATGACCTCTGTGGCCTCTACGTTTACACCGGTGACCGGTGGTTTTG
TGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAAGTCTATGAGTTCAGATGCTCCAATGCC
ATTCACTTCTCAGCAAGAGTCCCTCTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTCTTGGGGAAACAAAGGTGAATGGGGAGGTAAAGGGGTAAATTTTGTG
ACTTAGCTTCTAGCTACTTCTCCAGCCATCAGTCATTGGGTATGTAAAGGATGCAAGCGTA
TTTCAATATTTCCCAAACTTTAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAA

090259.071001

FIGURE 62

MGTLGQASLFAPPNGYFWSHSDHSAFCFAESCEGQPGKVEQMSTHRSRLITAAPLSMEQRQPWP
RALEVDSSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCCLLRLLDDLFILVEPSHKKEHYLSSVNKTGMTYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPDPRESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAAQAFNITSQDDVLFAlFSKGQKQYHHPDSDALCAFFIRAINLQIKERLQSCYQGEEN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTGSGKLLKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNRYRLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

000025.074001
10070.522000

FIGURE 63

AGGCTCCCGCGCGCGCTGAGTGCAGACTGGAGTGGGAACCGGGGTCCCCGCGCTTAGAGAAACGCGATGACCA
 CGTGGAGCCTCCGCGGAGGCGCGGCCGCGACGCTGGGACTCTGCTGCTGGTCTGCTTGGGCTTCTGGTGTCTCC
 GCAGGCTGGACTGGAGCAGCCCTGGTCCCTCTGCGGCTCGGCCATCGACAGCTGGGGCTCGAGGCCAAGGGCTGGA
 ACTTTCATGCTCGGAGGATTCACCTTCTTGATCTCTCGGGGCTCCATCCACATATTCCGCTGTGCCAGGGAGTACT
 GGAGGAGCCGCTCTGTAAGATGAAGGCTCTGGGCTTGAACACCTCACCACTATGTTCCGTGGAACTGTGACT
 AGCCAGAAAGAGGCAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCTCTGCTCCTGATGGCCCGCAGAGATCG
 GGCTGTGGGTGATTCTGCTGCTCAGGCGCCCTACATCTGCAGTGGAGTGGACCTCGGGGCTTGGCCACCATCAACTTCGAGT
 TCCAAGACCTTGGCATGAGGCTGAGGACAACTTACAAGGGCTTCAACCAGACCTGGACCTTATTTTGAACACC
 TGATGTCTCAGGGTGGCTCATCCAGTACAAGCTGGGGGACCTATCATTTGCCGTGAGGAGTGAATGAATATG
 GTTCCCTATATAAAGAGCCCCGCATACATCCCTACGTCAGAAGGCATCGAGGACCTGGGCACTTGTGAACCTGC
 TCTGACTTCAGACAACAGGATGGGCTGAGCAAGGGGATTTCCAGGGAGTCTTGGCCACCATCAACTTCGAGT
 CAACACACAGAGCTGCAGCTACTGACCACTTTCTCTTCAACGTCAGGGGACTCAGCCCAAGATGGTGTGAGT
 ACTGGACGGGGTGGTTTGAAGCTGCTGGGGAGGCGCTCACAATATCTTTGGATTCTTCTGAGGTTTTGAACCCGT
 CTGCCATTGTGACGCGGCTCCTCATCAACCTCTACATGTTCCACGGAGGCACCACTTTGGCTTCATGAAATG
 GAGCCATGCATTCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGCTGTGCTGACAGAAAGCCGCG
 ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTGGCTCCATCTCAGGCATCCCTCTCCCTCCCCCAGCTG
 ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGAGCCCTCAAGTACC
 TGGGGGAGCCAATCAAGTCTGAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTT
 TCGGGTACATTTCTATGAGACAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTCATGATCGGGGGCAGG
 TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCTTGATCCAGGGT
 ACACCGTCTGAGGACTTCTGGTGGAGAACTCGTGGCGAGTCAACTATGGGAGAAATTTGATGACACGCGCAAG
 GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAACTTCAGAATCTATAGCTGGATATGAAGAAGA
 GCTTCTTTCAGAGGTTCCGCTGGACAAATGGNGTTCCCTCCCAAGAACCCACATATACCTGCTTTCTTCTTGG
 GTAGCTTGCCATCAGCTCCAGCGCTTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGTTGTATTCA
 TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGAACCCAGAGAAGCGCTTTAATCTCCAGGTCCCTGGTGA
 GCAGCGGAATCAACAGGTATCGTTTGTGAGGAGACGATGGCGGGCCCTGCATTACAGTTCACGGAAGACCCCTC
 ACCTGGGCAGGAACAGTACATTAGTGGAGCGGTGGCACCCCTCTCTGCTGGTGCCAGTGGGAGACTGCGCCCTC
 CTCTTGAAGCTGAAGCCTTGGCTGCTGCCCAACCCCTCACTGCAAAAGCATCTCTTAAAGTAGCAACCTCAGGG
 ACTGGGGCTACAGTCTGCCCCCTGTCTCAGCTCAAAACCTTAAGCCTGAGGGAAGGTGGGATGGCTCTGGGGC
 TGGCTTTGTGATGATGGCTTCTCTACAGCCCTGTCTCTGTGCGAGGCTGTGCGGTGTCTCTAGGGTGGGAGC
 AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGACCCGAGCTCACAGCCC
 TGCAGCATCTGCTGACTCAGCCTGCTCTTTGCTGGTTCTGGGAGGCTTGGCCACATCCCTCATGGCCCAT
 TTTATCCCCGAACTCTGGGTGTGTACCAAGTGTAGAGGTTGGGGAAGGGTGTCTCACTCAGCTGACTTTGT
 TCTTCTTCAACCTTCTGAGCCTCTTTGGGATTCTGGAAGAACTCGGCTGAGAAACATGTGACTTCCCTT
 TCCCTTCCACTCGCTCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCTCACCTCGCTCTTCC
 CAGTTAGCAGTGTCTCTGGTGTCTCAGTGAGGAGACATGTGAGTCTCTGGCAGAAGCCATGGCCCATGTCTGCA
 CATCCAGGAGGAGCAGAAAGCCAGCTCAGATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGACATCTCAGGAGGAGG
 AGGAGGAGCAGAAAGCCAGCTCAGATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGACATCTCAGGAGGAGG
 ACAGAAGGCCAGCTCAGTGGCCGCCCTCCCAACCCCCACGCCGAAACAGCAGGGGACAGCAGCCCTCTTTC
 GAACTGTGCCAGTCCGATTTGAGCTTGTCTGGGGCCAGCCCAACCTGGCTTGGCTCACTGTCTCTGA
 GTTCAGTAAAGCTATAACCTTGAATCAAA

100770.6522066

FIGURE 64

MTTWSLRRRFPARTLGLLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHVFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDPSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTAEVDLYFDHLSRVVPLQ
YKRGGPPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKGSLSGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVMMEYWTGWFDSWGPHNILDSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYIILE
TSITSSGILSGHVHDRGQVFVNTVSI GFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLS SGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
 CTGGTGAGGGTTCTCTACTTGGCCCTTCGGTGCGGGGTCAAGACGCGAGGCACCTACGCCAAAGG
 GGAGCAAAGCCGGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
 CGACACGTGACGGTCTGTCCCGCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
 AAGAAGCTGTCCGTGCTTCGTTCCTGTCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA
 GGCAGACACTCGTTCGTTCGTAGTGGATAGGGGTCTATGACCGGTTCTCCTAGACGGGGCCC
 CGTTCGCTATGTCTTGGCAGCCTGCACCTACTTTCGGGTACCGCGGGTCTTTGGGCCGAC
 CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTA
 CCACGAGCCACAGCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTATTGCTTTTCTGA
 ATGAGGCAGCTCTAGCGAACCTGTTGGTCTACTGAGACCAGGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACTGAAATTCATCTAAGAACCTC
 AGATCCAGACTTCTTGGCCGAGTGGACTCTGGTTCAAGGTCTTGTCTGCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTCAAGTGGAGAATGAATATGGTAGC
 TACAGAGCCTGTGACTCTCAGCTACATGAGGCACTTGGCTGGGCTCTTCGCTGCACTGCTAGG
 AGAAAAAGATCTTGCTCTTACCACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
 GACTCTATACCACGTGTAGATTTTGGCCCAGCTGACACATGACCAAAATCTTTACCCTGCTT
 CGGAAGTATGAACCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTCACTGTAACCAAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
 AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGTCTCTCGAGATGTCATCAGCAAGT
 TCCAGGAAGTTTCCTTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGGCCCCGCTGGGCCCAT
 TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
 GAACCTATATGACCCATACCATTTTTGAGCCAAACCAATTCCTGGGTGCCAAATAATGGAGTC
 CATGACCGTGCTATGTGATGTTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG
 AGACAACTATTTTTGACGGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCTGTTGAAGCCACCAATTCCTG
 GGGCAAAACATCCTTACCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
 GTGGTTTCCCTCCAGTTGCCAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
 ACTCCAAACATTTCCAATTTTAGGCTCAGTTGGGGACATTTCTATATCTACCTGGATGG
 ACCAAGGGCCAAAGTCTGGATCAATGGGTTTAACTTGGGCCGCTACTGGACAAGCAGGGGCC
 ACAACAGACCTCTACGTGCCAAGATTCTGTCTGTTTCTAGGGGAGCCCTCAACAAAATTA
 CATGTCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCCTATC
 CTCATAGCACTAGTACTTTGCAAGGACATATCAATTCCTTTCAAGCTGATACATCAGT
 TGCCCTCGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCTGTTGGCTCATGC
 CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA
 CCAGCTGGCCAACTATGTGAACCCCGTCTCCACTAAAAATACAAAATTAAGCCGGCGTG
 ATGTTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
 AGGAGGCAGAGGTTGCACTGAGTGGAGGTTGTACCCTGCACTCCAGCCTGGCTGACAGTGA
 GACATCCATCTCAAAAAA

00002759-071001

FIGURE 66

MAPKKLSCLRSLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVI
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALNLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDDGPEGLKCGSLRGLYTTVDGFPADNMTKIF
TLLRKYEHPGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGLPPSPKMMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSDDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWFPYQAPSGPTFYSKTFPILGSVGDTFLLYL
PGWTKGQVWINGFNLGRYWTQKGPQQTLYVPRFLLFPFRGALNKITLLELEDVPLQPQVQFLD
KPIILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTTCACATGGTAGACCAGTATGACCAGCTATATTTCAAGCGTTTTTGGTGTGTT
CTTGTGCAGAAGTTAGTGAAAAATAAACTTAGGGAAATTAGTTTGAAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTGCGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCAGAAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCCTTCACGTGAAGTTCACGTGATGTGGCTGAAATTCCTGCTGGGTGTATTGTCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTTCATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAAATGATGAATGTCGCTGAGCTGGAATCCAGA
ACTGTGAGCTAGAGAGAAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAAACGACT
GACTTGTTTTAAAAATTATGGCATAACAAAATGTTACTATTCTCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTTATTTCTCTAACCAACAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGACCGCCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTTGTATACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCTTTTGCAAAATGGGATTTAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCATGTTTGTAGGGTTTTAAGTCATTCATTTCCAATCATTTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTCTTTTTAAATTGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAAAA

10070-552060

FIGURE 68

MAYMLKKLLISYISIIICVYGFIPLYTLFWLFRIPLKEYSF EKVREESSFS DIPDVKNDF AFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTF EKLRQHISR NAQDKQELH LFM LSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELH LCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNL NSENNKMIGLESRLRELRLHLKILHVKS NLTKVPSN
ITDVAPHLTKLVIHNDG TKLLVLNLSLKKMMNVAELELQNC ELERIPHAIFSLSNLQELDLKS
NNIRTIEEII SPQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRLCDVS YNNISMIP EIGLLQNLQHLHITGNKVDILPKQLFKCIKLR TLNLGQNCITSLP
EKVQQLS QLTQLELKGNC LDRLPAQLGQCRMLKKSGLVVEDHLFD TLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

10070-55360

FIGURE 69

CCCACGCGTCGCGCCTTCTCTGGACTTTGCATTTCATTCCTTTTCATTGACAAACGACTTTTTTATTTCTT
TTTTTTCATCTCTGCGGCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTGTGTTTTACACACATAAGGAT
CTGTGTTTTGGGTTTCTTCTTCTTCCCTGCATTGGCATTGCTTAGTGGTTGTGTGGGGAGGAGACCAAGTGG
GCTCAGTGCTTGTCTGCATCTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGTATATGCTGTGTC
ATCGTCTGGTGTATCCTGCGGCCCTTGCTCCTGCTGATAGTTGTGCTGCTCTGTCTTTTACTCTCAAAATACACAAC
CGCTCAAAAGCTCGAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCAACAACCAGACAGGTGTGGTGGGCCAAG
AACAGCCAGGCCCAAAACCTTGCCACGGAGTCTTGCTCCTGCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC
AGTTTTGTATCCTCTGCCACCTTGTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCNAATGAGGCCACCTGTTTGTGATGTGCAGGCA CAGAAGAAAGGCCACAG
CTCCCATCAGTTTTCATGAAAAATAACTCAGTGCCCTGCTGGGAACCAAGCTGTGCGAGATCCCTACAGAGAGCTTC
CACTGGGGCCAAACCTTCCAGGAAGGAGTTGGGGAGAGAGAAACCTCACTGTGGGGAATGCTGATAAAACGATCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACCTGACGTTTCCCTGGAGGTTCCAGAAA
GCTGATGTAAACACAGAGCCTATAAAAGCTGTGCGTCCCTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCCCTCTTAATTTCTCTCCTGTTTGGCGAGCTGACAAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAAATATGGCAGAGACCCACAAAGCCATGATCTCTGCAACTCAATCCC
AGTGAGAAGCTGCACCTGGACAAATAGAAAGACCAGAAAACAAAGCCATGATCTCTGCAACTCAATCCC
GATCCAGATGGAAGCTGTGAAAGTGAAGACATTAAAGTCTTTGACGGAACTCCAGCAATGGGCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTCCGTGATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTCTACT
GACTCAGCAAGAAATTCAGAAAGACTGTCTTTGTCTTCTACTACTTCTCTCTCTTAACATCTCTCTTCCAACTGT
GGCGGTTACCTGGATCACTTGGGAAGGATCCTTACCAGCCCCAATTACCAGGCGCATCTGAGCTGGCTTAT
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACCTTCAAAGAGATTTTCTAGAAATAGAC
AAACAGTGCAAAATTTGATTTTCTTGCCATCTATGATGGCCCTCCACCAACTCTGGCGTGAATGGACAGTCTGT
GGCGGTGTGACTCCCACTTCGAATCGTCAATCAAACTCTCTGACTGTGCTGTGTCTACAGATTTATGCCAATTTCT
TACCGGGGATTTTCTGCTTCCACACCTCAATTTATGCAGAAAAACATCAACACTACATCTTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAAATCTACCTAGAGGCTTTAACTCTAATGGGAATAACTTGCACATCAAA
GACCCAACTGCAGACCAAAATATCAAATGTTGTGGAATTTTCTGCCCTCTTAATGGATGTGGTACAAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCTCAAATCTGAAGTGATCAAC
CGTCAGAAACAACTCCAGATTATGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGCAATATAAACACCAAGCATGGGCTCTTTTGAATCCAAATTC
TTTGAAGAGACTATACCTTGAATCAACATATTATGTGGATTTGAACCAAACTCTTTTGTTCAGTGTAGTCTGCAC
ACCTCAGATCCAAATTTGTGGTGTCTTGTATACCTGTAGAGCCTCTCCCACTCTGACTTTGATCTCCAACT
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAACTTGTAAAGTGTATCCCTTATTTGGACACTATGGGAGA
TTCAGTTTAAATGCCTTTAAATTTCTTGAGAAGTATGAGCTCTGTATCTGCAGTGTAAAGTTTGTATGTGAT
AGCATGTGACCCAGTCTCCTGCTCAATCAAGGTTGTGTCTCCAGAAGCAACGAGACATTTCTCATATAAATGG
AAAACAGATTCATATAGGACCCATTGCTGTAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTCAGCAT
GAAACACATGCGGAAGAACTCCAAACGAGCCTTTCAACAGTGTGCATCTGTTTCCCTCATGGTTCTAGCTCTG
AATGTGCTGATGTAGGACCAATCAGGTGAGGCATTTTGTAAATCAACGGGACAGTCAAAATACCGAAGCTG
CAGAACTATTAACTAACAGGTCACCACTCAAGTGACATGTTTCTCCAGGATCCCAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAAATGAGGAAGGGCTGAAAGTGACACACAGGCTGCATGTAAAAAA

FIGURE 70

MELVRRLLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSIVQLDDPGSCSEENIKVFDGTSSNGPLLGGVCSKN DYVPVFESSSTLT
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDLTLGSGFTSPNYPKPHELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRV IISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQQLQIIVKCEMGNST
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTI LESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCVKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLI CDSSDHQSRCNQGCVSRSKRDISSYKWKTD SIIGPIRLKDRSASGNSGFQHETHA
BETPNQPFNSVHLFSFMVLALNVVIVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

100120-652000

FIGURE 71

GACGGAAGAACAGCGCTCCCCAGGCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCGCGTTGCTGCTGTTGCTGTTGCTGC
TGCTGCCGCGCCGCCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC
CTGGACGCGCCGCGAGCTGCCGCGCTGGTTTGACCAGGCCAAGTTTCGGCATCTTCATCCACTG
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAAATTTATGAAAGATAATTACCCCTCTAGTTTCAAATATGAAGAT
TTTGACCACTATTTACAGCAAAATTTTTAATGCCAACAGTGGGCAGATATTTTTTCAGGC
CTCTGGTGCCAAATACATTTGTCTTAACCTTCCAAACATCATGAAGCTTTTACCTTTGTGGGGGT
CAGAATATTCTGGAACTTGGAAATGCCATAGATGAGGGGCCAAGAGGGACATTTGCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGACTGTACTATTCCTTTTTTGA
ATGGTTTCATCCGCTCTTCTCTGAGGATGAATCCAGTTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACC GGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCAGTTTCGGGGCACAGTAGTCACCAATGATCCTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCGAGTATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACATGCATGACAAATAGACAACTGTCTTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCACACTAGATGGCACCATTTCGTAGTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCGAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT
CCCCAAGCTATTTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTGAAGTGCACAGCTAACCATTCATCAGATGC
CGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACATATCAGGTGTCTATAATTGTAGCATATGGAGA
AAGCAATGTAACTGGATAAGAAAATTTATTTGGCAGTTCAGCCCTTTCCCTTTTTCCCACTA
AATTTTTCTTAAATTACCATGTAAACCATTTTAACTCTCCAGTGCACCTTTGCCATTAAAGTC
TCCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTTGCCAAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAATACTGTAAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAAGTGAAGCTAGGACACTACATTATAAAAAAA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAA
GTTTTCTCTTCTCAATTATAAATTAACATAAGTGTACTGTAACCTTTACAACAGTTTAAAT
TTTTAAACCTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAACATAAACTCATTTGTGCAA
ATGTAA

03002759.071001

FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPWTWESLDRQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW
FHPFLFEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDDGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

100120.652060

FIGURE 73

AGCAGGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGAAGTATTATGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGACAGAGAGCT
TTCCATCCAGGTGTCTATGCAGAAATTATGGGGATCACCTTTGTGAGCAAAAAGGCGAACAGC
AGCTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGGAGA
TGGATTCTGGTCTCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCGTATTTGGAAGGTTCCAGTGAGCGACAGTTTGCAGCCTATTGTTACAACTCATCTGAT
ACTTGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCA
AACTGCAACACAAACACAGAATTATTGTGAGTGACAGTACCTACTCGTGGCATCCCCTT
ACTCTACAATACTCGCCCTACTACTCTCCTCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTGATTGTTGTGCACAGAAAGTTTTATGGAACTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGTCTGCTCTCCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGATTGTC
TATGTCAAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGA
AAACTGATAAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACCTACCGTGCATGCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTCTTCTTATGCTCC
TTACCTTGCCCCAGCTGGGGAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCTT
GGTTCCTAAGTGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGGAATGC
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCCTGGGAGAAAGGAGTTTGTCAAAGTGCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAAGGACTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGAC
CCTTTCTTCAAGCTCTGAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTA
AGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGGCTAAAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAACTCTTATAAATTTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTC
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATCTCTCAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCA
GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTATTTTGTGAGACTAATCTT
ATTCATTTTTCTCTAATATGGCAACCATTAACCTTAATTTATTTAATACATACCTAAGAAG
TACATTTGTTACCTCTATATACAAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTTCCAAAGAGGACTGAGAGATGCAGAAATATTGTTGACAAAAAATTA
AGCATTAGAAAACTT

10072050.071000

FIGURE 74

MARCFSLVLLLSIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETETPFVENKAAPKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAPFPFTKNQKQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

100120.6222060

FIGURE 75

AGATGCGGCTCTTGGCACCTCTAATTGCTCTCGTGTATTCCGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCTTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCCACCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCCGAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTGTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCATAGTGTTC
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAAGTGAACGGGACAAGAGGGTCACCTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAACAT
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCTGATCCTGTTC CAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGA CAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCAACACAGTGTGAGA
TGGGGAAAACAAGAAGGATAAAATAGATCCTCACTTTGGCAGTGCCTTCTCTCCTGTCAATT
CCAGGCTCTTTCCATAACCAACAAGCCTGAGGCTGCAGCCTTNNATNNATGTTTCCCTTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTGAG
GCACCCATACAGGAAGGCCTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC
AGCTATTGAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCTTCTTAG
TTGACCTGCACAGCTTGTTAGACCTAGATTTAAACCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAAITTTCCCCCAAGGACTTGTCTTCTTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGAATTTAC
TAACCTCTGACATACTCCCAACCCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATT
TCCTTTTG

100170.652060

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSPLTQQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

0002259.071001

FIGURE 78

MGLLLLVPLLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDPQSRLYGVICYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

100120-6522060

FIGURE 80

MMWRPSVLLLLLLLLRHGAQ GKPS PDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTP EESQARLGRI VDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

030259.07001
100720.642060

FIGURE 81

GGGGCCTTGCCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCAG
CCTGTCTGTGTCGTGTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGAATTTGGCCGCGAGGCGCTCCAGACCTAGAGGGGCGCTGGCTGGAGCAG
CGGGTCGTCTGTCTCTCTCCTCTGCGCCGCGCCCGGGATCCGAAGGGTGCAGGGGCTCT
GAGGAGGTGACGCGCGGGGCTCCCCGACCTTGGCCTTGCCCGCATTCTCCCTCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCAATGTCGCGAGCCTGGATCCCCGCTCTCGGCTCGGTGTG
TGTCTGCTGTCTGTCGCGGGGCCCCGCGGCAGCGAGGAGCGCTCCCATTGCTATCACATG
TTTTACGAGGCTTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCC
CTCTTGAGGAATTTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTTACAGTAATAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCCGAGAAAGAACTGG
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTTAATTTACAGAAGAATTTGTTGGAAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCAACATGTGGGCCTTGTTCAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA
AAACTTTACATCAGCCAAAGATGTTTTGTTTGCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAAAATCTTCACGGTAGATGCTGGA
GTAAGAAAAAGGATCCCCAAAGTGGTGGTGGTATTTATGTATGGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTATAGTTTCTGTGGCCA
AGCCTATCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGGCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCCGCTC
ATGCTTGAATTTGTTTCCAAATAGCCAAGACTTTTGAATCTCGGCATTTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTATGATCAGCGCAGGAGTTCAGTTTCACTGACTATAGCACC
AAGAGATATGCTTAGCTGTATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCTTAGTAATTTGCACAGATGGGCAGTCTCTATGATGATGTCCAAGGCCCTGCAGCTGTG
CACATGATGCAGGAATCACTATCTTCTCTGTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCAAGAGAGTTTACAGGATT
AGAACCAATTTGTTCTGATGTCATCAGAGGCATTTGTAGAGATTTCTAGAAATCCAGCAAT
AATGGTAAACATTTTGACAACTGAAAGAAAAAGTACAAGGGATCCAGTGTGTAAATTGTATT
CTCATAATACGAAATGCTTTAGCATACTAGAATCAGATACAAAATATTAAGTATGTCAAC
AGCCATTTAGGCAATAAGCACTCCTTTAAAGCCGCTGCCTCTGGTTACAAATTTACAGTGT
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAACACTTAAAGAGTTCTAACCATGCCTACTCAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAACTGTACTTAGACCAAAAAAAAAA

100170.6522666

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLLEEFVSY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCHEQMMCSKTCYNSVNI AFLI
DGSSSVGDSNFRMLLEFVSNI AKTPEISDIGAKIAAVQFTYDQRT EFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

100120.65220000

FIGURE 83

CGCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCGCTCCCGCATCTGCACCCGCGAGCC
GGCGGCCCTCCCGCGGGAGCGAGCAGATCCAGTCCGCGCCGCGAGCGCAACTCGGTCAGCTCG
GGGCGGGCGGCTCGGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGGCCACCTGCTGTGCCTGC
TGCTGGCGGGCGGGTCCCCACGGCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTGC
AAGCCCGCGCCGGCTCTCAGCTACCCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGTGTATGGAGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACTTACCTCCAGCTAT
CACAATGAGACCAACACAGACAGCAAGGTTGGAAATAATACCATTCAATGTGCACCGAGAAAT
TCACAAGATAACCAACACAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCATCTGTG
TGGAGACGAAGAAGCGAGAAGGACGACGAGTGCATCATCGACGAGGACTGTGGGCCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACAAACAGAGGGAAGTCCAGCCGGGGCTG
TGCTGTGCCTTCCAGAGAGGCGCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGGACGCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTACA
TCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC
TCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGACGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCCTTACCAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAACCAATGTGG
AGTCTCCCTCTGATTGGTTTTTGGGAAATGTGGAGAAGAGTCCCTGCTTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTTCCACGCACTTCTTCCATGGGCATAGGTAAGCTG
TGCCCTCAGCTGTGTGCAGATGAAATGTTCTGTTCAACCTGCATTACATGTGTTTATTTCATCC
AGCAGTGTGTGCTCAGCTCCTACCTCTGTGCAGGGCAGCAATTTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGCGGAGGGGTCATTGTTCTCCTGTCATCAGGTCATCGGAGTCTCAG
GCTCAGAGACTGCAAGCTGTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACAGCCCTGGTGCCACCAA
AAGTCTCCCCAAAAGGAAGGAGAAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACTAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC
AGTGTGGGCGAGCCGCTCTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGTAATTGTAGGGCGAGGATTATAAATGAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAAATTACAACACGCTGGAGAAAATCAAACGAGCAGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTCAGGTGTCA
TGGAGCTGTGGCCACCATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATGTGA
TAAGCATGCTTTCTTGAAGTTTAAATTTATGTATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAATCACTTCACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

100720-6542060

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEAAAASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQQRMLCTRDSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGGCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

0902759 071003

AAGGAGGCGCTGGGAGGAAAGAGGTAAAGAAAGGTTAGAGAACTTCACTTCATCTCTCGGGCTCAGAGAGCACTCTG
AAGATAACAATAATTTTCAGCCCACTCCACTCTCCCTCCCTCCAAACAACATGTGCATGTACACAACACATACA
ACACATACATACCTTTCTCTCTTCACTGAAGACTCAGAGTCACTCACTCTGTGAGCAGGTCTAGAAAAGAGCAC
TAAAGGCTTTAAGGACAGGCGCTGGCCAGCTCTCTCGAGCTCTCTTGGCTTGTGAGTTCAAAACAATCTGGAGGCG
CCAGGCACGGTGACTACACCTGTATTCACGATTTTGGGAGCGCGAGGTACGAGCATATCTTAGGTCAAGGTG
TTCGAGACAGCTTGGCCACATCGAGAAAGACCCCACTCTACTAAAAATAAAAAATAGCCAGGATCGGTGGC
AGGTGCCTGTAAATCCAGCTACTACAGTGTGGCTGAGCCAGGAGAAGCTGGTAATCCAGAGAGCGGAGGATGCGGT
CAGCTCGAGTGCACCGCTGCATCTCAGGCTGGGTGACAGAAATGAGACTGTGCTCAACAAACAACAAACACCGGAGG
GGGTGAGTAGTACTGCTTCTCTCAACCTCTTAACTCTGCATCTCTCTCTCCAGGCTGGCCCTGTAGGGCGCTCT
GCATAGCTAGAGCAGCCGACCCGAGGAGACAAGGAAGAAGGACATATTGAGGGGGACGAAGTGTGACGCCCT
GTGTAGAATGACTGCCCTGGGAGGGTGTTCTCTTGGGCCCTGACGGGTTGTGACCTTTACCTGTCAAAACACA
AAGAGCAGGACTCAGACATCTCTTGTGAATGGTCCCTCGCTCAGCTCCACATGAGGCTCTCTGTGCGCCCTC
ACTCTTCTTAGCTTGGGTGGCTGGTGCCTGCACTGCACTGTGCCCGTGTATCTCGCATCTTCTCTGCCCCCTC
GTGTGGCTCGCAGATCGCGCCCTGGTATACGCCCGCTGTCTACCCGCGAGTACCTCAACCTGTGAATGTCAATGA
CTTATTCTCTGACGGCGACTCCCCGGCACTCCCGGACGACACAGACCTGTCTCTGTAGAGACAACGATATTGT
CCGTGTGGACAGAGTAGGTGGCTACTCTGGCCAACTCACAGAGCTGGACCTGTCTCCAGAACAGCTTTTGGGA
TCCCGGACAGTGTGATTTCCATGCTCTGCCCAAGTGTCTGACCTGCACCTTAGAGAGAACAGCTGACCCGGCT
GGAGGACACACAGCTTCTCGAGGCTGGCCACGTCTACAGGAATCTATATCAACCAACCACTGTACCGCATCGC
CCCCAGGCGCTTTTCTGGCTCAGCAACTGTCTGGCGTGCACCTCAACTCAACCACTCTGTAGGGCGATTGACAG
CCGCTGTTTGAATGTCTGCCAACTCTGGAGATACCTTGTGTGGGGCAACAAGGTATGATGCATCTCTGCACAT
GAAGTCTCGGCGCTCGCCACACTCGGTAGACTGTGTGTAGGACATGAACCTGTGGGAGATCTTCGCATATTGC
CTCTGAGGGGCTCGAAAGCTGGAGAGCTCTCTCTTTATGACAAACAGCTGTGGCCGGGTTGCCAGCGCGGCAT
GGAACAGCTGTGCCGGCTCAAGTTCTTAGACTCAACAAGAACCCGCTCCAGCGGCTAGGGCCGGGGGATTTGC
CAACATCTGCACACTTAAAGACTGGGACTGACAAACATGAGGAGGTGTGTTCCATCGACAAGTTTGGCTGTGT
GAACTCCCGCGAGCTGACCAAGTGCAGATCACCAATAAACCCGCTGTCTCTATCCACCCCGCGCTTCC
CCACTGTGCCCGAGATGGAGACCTCATGCTCAACAACAACCGCTCAGTGTCTGTGCACAGCAGAGCGTGAAGT
CTCTGCGCAACTCTCAGGAGGTTAGTCTCCAGCGAACCCCTCCGCTGTGACTGTGTCAATCCGCTGGGCCATATG
CAGCGGCACCGCTGTTCGCTTCTCAGCGCGCAATCCACCTGTGTGGCGAGCTCCGACCTCAGCGCTCCCC
GGTCTGTGGAGTGGCCCTTCGGGAGATGACGGGACCACTGTTTGGCCCTCATCTCCCAAGAGCTTCCCCCAAG
CCTCCAGGTAGCAGTGGAGAGGACGTGTGTCTGCACTGTGGCGCACTGGCCGAAACCGGAATCCGAGATCTACT
GGATCATCGAGCTGGGCTCTGCATGCACATCTGCCCATCAGGCGAGGAGTACCGGTTGTACCCGAGGGGACCT
GGAGCTCGGGAGGTTGACGACGAAGAAGGACGGGCTATACACTGTGTGGCGCGCAACTGTGTGGGCGCTGACAC
TAAAGCACTTATGTGTGTGGCGCGTCTCTCTCTCAGCAGGCGAGGAGCAAGAGCAGGCTGTGAGCTCCG
GTGTGAGGAGACCCAGCTTATCATCATCTGCTATTGTGGGTCACCCCACAACAGTGTCCCAACCAACTCAT
CTGTGTCCAGTCTCTCTCTCCGGGSCAGGGGGSCACAGCTGTGGCGGCTCTGCTCTGGGAACTCAACAGTCA
CAACATCAACCGCCTCTCTCAGGCAACGAGATCTGGGCTGTGCTCAAGTGGCTTTGTGCTAGTGCCCAACCCA
TGTGGCTTGTGTATGGGCGAGGACAAGAGGCCATCTTGGCCAGAGGCTTAGGGAGATGCTCTGGGCTCAT
TGCATCTCTGGCTCTGCTGTCTTCTCTGGCAGTGGGCTGGGCGCCACTTGGCAACAGCCACACCGAAG
GGGTGTGGGTGGGAGCGGCCCTCTCCCTCAGCTCTGGGCTTCTTGGGGCTGTGATGTGCCCTCTGTCTCGGTTGT
GTGTGCTCCCTCGTCTGCCCTGGAATCCAGGAGGAAGCTCGCCAGATCTCAGAAGGGGACAGTGTGGC
ACCATTTGTCTCAAAATTTCTGAAGCTCAGCTCTCTCTCAGCATAGAGAATCATCAGGATCATTTTACAAA
AGAGAAGCAGTCTGGGCGAGTATGCCCTCGAGAAAGGACATGGACACATGCTCTGTAGGCTGTGAGCTGGGCG
CAGACAGCAATGGGGCTTTGTGGCCCTGGGGGCTGCTTCTCAGGCTTGAAAAAGTTGCCCTTACTCTCATTGGGTCA
CCTCTGTGTCATCTGAGGAATCTTCAAGGAACAGGAGGACTTGTGCTAGAGCTCTCTGGCTCTCCCATCTTCT
CTCTCTGCGCCAGGCTCTCTGGGCTGTGCTTGTGCTTGTGCTCTGGGCAAGGCTGAAGGAGGAGCTTCATCTCAT
CTCGGGGGGCTGCCCTCAATGTGGGAGTGACCCACGCGAGATCTGAAGAGCAATTTGGGAGAGGAGTGGCCAGGA
CGCTCATCTCAGACGCTGGGCTGGCATCTCGAAGCTGACTTCTATAGCAATTTTGTACTTTTGTGTGGAGAA
ATGTGTCACTTCCCCAACCGATTCACTTTTCTCTGTTTGTAAAAAATAAAAAATAATAAACAATAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLQSNISVRVDQSELGYLANLTELDLSONSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSAFGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAIILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLPL
ELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNAALSALHQQTVESLNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPDQLQRLPVREVPFREMTHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLLTPAHAGRRYRVYPBGTLELRRVTAEAGLYT
CVAQNLVGADTKTVSVVVGRRALLQPRDEGGGLELRVQETHPHYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAIALALAVLLLAAGLAAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSRRVV
SAPLVLPWNPGRKLPSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

100770.65220660

FIGURE 88

MRQTIKVIKIFILIIICYTVVYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLEHLFMLSIGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLBELHLTLGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKMANLTELIRCDLERIPHSIFSLHNLQEBIDLKDNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

100120.6520660

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCCTGAACGCAGGAGCTGTCATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAGTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTTGGAACTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCTTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATT CAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTCCGGTGTCTCTCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACTAAAAGCACTCCCA
CGTCTACAATGGAGTTCAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTGAGCGC
CACGTGAGACACCTACAACGAGATGCCCTTAAGCCAGCTCATGAATGGCCCCCATCAGAAAGAA
GCTCAAAATTAATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCGTG
GGTGCCGAAACTGAAGTGCCAGAACTGCCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCTTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTAATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

100120*65220660

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGGLYRE
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPBPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMAKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

100170.652060

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGCGCGCGCCGTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCCTGGG
CACTCAGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTGTAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

000275.07001

FIGURE 92

MGARGALLLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCVGSLLSHRWALTAACHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWSVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACGCGTCCGCGGACGCGTGGGAAGGGCAGAA**ATGGG**ACTCCAAGCCTGCCTCCTAGGGCT
CTTTGGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCTCTGGGCCGTGCGGACCTTGAGGAAGAGCTGAGTCTCACCTTT
GCCCTGAGACAGCAGAATGTGGAAGACTCTCGGAGCTGGTGCGAGGCTGTGTCTCGGATCCGAG
CTCTCCTCAATACGGAATACTCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGCTCTGAGTTTCATCACTATGTGGGAGGACCTACGGAACCCGATGTTGTAAAGTCCCCAC
ATCCCTACAGCTTCCACAGGCCCTTGGCCCCCATGTGGACTTTGTGGGGGACTGCAACCT
TTTCCCCAACATCATCCCTGAGGCAACGTCTTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACAACTTGACCTCACAAGACGTGG
GCTCTGGCACCGACAATAACAGCCAAGCCTGTGCCAGTTCTCGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTTCATGCGCCTCTTCGGTGCGAACTTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGT
GGGGCCGGGTGTGGTCTGTCTCTGGAAGACACCACTTCCGCCCTACCTTCCCTGCCTCCAG
CCCCATGTGCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCAGAAATGAAA
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGCGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTTGAGCTCTAGCCCCACCTGCCACCATTCCAGTTACTTCAATGC
CAGTGGCCGTGCCATCCACAGATGTGGGTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGGCCATTCCATGGGTGTCTCGGAACCTCGGCCTCTACTCCAGTGTTTGGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGCCGCGCCCCCTCTTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCGAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTCT
TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGTCTGGTCTGGCTGGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCAGCTTTGCT**G**AAGACTCTACTCAACCCCTGACCCCTTCCCTATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTTCTGCCCTGTTG
GAAGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGTGAAA
TGCTGTGAGCTTGACTTCACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCTTAGATTCTCTCAATAAGATGCTGTAAGTACTGATTTTGAATGCCTCTCCCTCCGC
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTACCGTTTACTCT
TTCTTACCCTGACATCCAGAAACAATGGCCCTCCAGTGCATACTTCTCAATCTTTGCTTTATG
GCCTTCCATCATAGTTGCCCACTCCCTCTCTTACTTAGCTTCCAGGTCTTAACCTTCTCTG
ACTACTTGTCTTCTCTCATCAATTCTGCTTCTTCATGGAATGTGACCTTCAATTGC
TCCATTTGTAGATTTTGTCTTCTCAGTTTACTCATTGTCCCCTGGAAACAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAA
TGTAAGAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRITLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGYKYLTLNVADLVRFSPITLHTVQKWLAAAGAKCHSVITQDFLTCWL
SIRQAEALLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMASAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDSDLSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPSSSYFNASGRAYPDVAALSDGYWVSNRVPPIPVWVGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGCTGCTCGGCGCGGAACAGTGTCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTTCTC
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCTCCCTGTGCTTGGCCCCAGTCTACCCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCTATAAGGGA
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAAGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTTCAGCATTTTGGGAAGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGTGCAACCGGCACCTGTTGGCAGAGAAGCATGTCTCACAGCTGCCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC
AAGTTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAA
ATTTCAAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTTCTC
TGGTTATGACAATGACCGACCAAGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTTCAGG
GCACCACTGGGTGGACATGAATGGTTCCTCCACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCCAGATTTGCTATTTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG
TGAACACAGTGTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC
AAATTGTTTTTTGTCAATTGGCGTGCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTACTATTTGAAAACCTG
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA
AAAAAATACTGATTGTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG
CAAACCTTGATTTTTTATTTCACTGAACTTGTTCAAAGATTTATATTAAATATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAAAAA

100170.652060

FIGURE 96

MAGIPGLLFLFLFLLCAVGQVSPYSAPWKPTWPAYRLFPVVLQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPGKWIKNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFGDVKDETYDLLYQQCD
AQPASGSGSVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

100720 6522066

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCCGCCCCACCCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCCTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCTGTGTATTCTTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTTGCCTATCTGCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGTCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTTGC
CCCACCTCAGACCTGCGAGAAGCTGAAGGTTCTTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCGCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCGGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGCCCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGCGCGGCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGGCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTTGTAAACCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT
CTCCAAAAAAAAA

0500275.0131
100120.6522060

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFSTLLLLASTAILNAAARIPVPPACGKPKQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLTTSRWVITAACHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWSIGWGSIQDG
VPLPHPQTLQKLKVPIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

100170-6520680

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGTGCGCCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC
AACAAGGAGCGCGGGCGCGCGGCGAGAATCTGTTCCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGC CAAGACAGAGAGGATC
GGCTGTGTTCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACCTCCCTCTGTGAACCCATCGGAAGC
CCGAAGATGCTCAGGATTTGCCTTACCTGGTAACCTGAGGCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGAACAGAGGTCTCAGGCTCCCTGGCAACCAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAATTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGTGAGTTGCCTCCTTCCAGTG
AGGTCTTGCCCTCAGTTTTCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCAAAGTCCCTGCCCAATTTCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTGAGGCTGAACTCGGGCCCTGGTCA GTGTGGGGCCCTCTCCTGGGA
CTACTGCTCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTGAGCTGTCTCTGTATCTTCCCACCTGTCCCCAGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCTTGAGGACACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCTGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAAGTGGGGAGGACGGGACGAGGGAAGGAAAGTAACCTCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

10110.512.060

FIGURE 100

MHGSCSFLMLLLPLLILLVATTGPFVGALTDEEKRLMVELHNLRYAQVSPITASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVLCNYEPGPNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTEVPSILAHSLSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGBLQATLDHTGHTSSKSLFNFNPNTSATANATGGRALALQSSLPGABGPDKPSVV
SGLNSGPGHVWGPELLGLLLPPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

100177-6525088

FIGURE 101

GTAACTGAAGTCAGGCTTTTCATTTGGAAGCCCCCTCAAAGAAATTCGGTCATTTCTCCAAGTTATGGTGGACGT
 ACTCTGTGTGTTCTCCTCTGCTTGCTTTTTCACATTAGCAGACCGGACTTAAGTCACAAACAGATTATCTTTTCAT
 CAAGGCAAGTTCATGAGCCACTTCAAAGCCTTCGAGAAGTGAACACAAATGAATTGGAGACCAATCC
 AAATCTGGGACCCAGTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTTGTGAAATCTCCCTGA
 ACATCTGAAGAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTACAGAGCTCCAAACTGCAAT
 TCCAGCCCTCAGCTCAAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACTCGGTGATTTTTCACAA
 TTTGGCCAAACACACTCTTGTGTTTAAAGCTGAACAGGAACCGAATCTCAGTATCTCCACCAGATGTTTAAACT
 GCCCAACTGCGCACTCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACATGACATTTCCAGGCCCTTGG
 TGCTCTGAAGTCTCTGAAATGCAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTTGACAA
 CATGGAAATTTTTCAGCTGGACCAATAACAACTTACACAGAGATTACCAAAGCTGGCTTTTACGGCTTGCTGTAGTCT
 GCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCTCGGGAGTCTTGCACAGAGCTCAG
 TGAGCTGGACCTTAACCTTCAATCACTTATCAAGGTTAGATGATTCAGAGCTTCCCTTGGCCTAAGCTTACTAAATAC
 ACTGCACATTTGGGAACAAACAGAGTCAGCTACATTGCTGATTGTGCTCTCCGGGGCTTTCCAGTTTAAAGACTTT
 GGATCTGAAGAACAATGAAATTTCTCGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAG
 GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCCTTCACGTGTTTGGATGCAATTTGGAGCA
 TCTAGACCTGAGTGACACGCAATCATGCTCTTTCAGGCAATGCAATTTTCACAAATGAAGAACTGCAACAAT
 GCAATTTAAATACATCAAGCCCTTTGTGCGATTGCGAGCTAAATGGCTCCACAGTGGGTGGCGGAAAAACCACTT
 TCAGAGCTTTGTAAATGCCGATTTGGCCATCCTCAGCTGCTAAAGGAGAAAGCAATTTTGTGTTAGCCCAAG
 TGGCTTTGTGTGATGATTTTCCCAAACCCAGATCAGCGTTCCAGCCAGAAACACAGTCCGGCAATAAAGAGTT
 CAATTTGAGTTCATCTGCTCAGCTGCCAGCAGAGTATCCCAATGATGTTTTCCTGGGAAAAAGACAAATGA
 ACTACTGCATGATGCTGAAATGAAAAATTTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACAC
 CATCTCTCGGCTCGCGAGGTTGGAATTTGCGAGTGAGGGGAAATATCAGTGTGTCATCTTCAATCACTTTGGTTT
 ATCTACTCTGTCAAAGCCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCAATGGATCTCACCAT
 CCGAGCTGGGGCCATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCACAGATAGCGTTGGCAAGGA
 TGGGGGCACAGACTTCCAGCTGCAACGGGAGAGACGATGATGATGCCGAGGATGACGTGTTCTTTATCGT
 GGATGTGAAGATAGAGGACATTGGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAATG
 AACCTGACTGTCTAGAAACACCATCATTTTTCGGGCCATGTTGGACGAACTGTAAACCAAGGGAGAAACAGC
 GCTCCTACAGTGCATTTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAGATGATAGCCCATTTGGTGGT
 AACCGAGAGGCACTTTTTCGAGCAGGCAATCAGCTTCTGATTAATTGTGGACTCAGATGTGATGCTGGGAA
 ATACACATGTGAGATGTTCAACACCCCTTGGCACTGAGAGAGGAACGCTGCGCTCAGTGTGATCCCACTCCAAC
 CTGCGACTCCCTCAGATGACAGCCCATCGTTAGACGATGACGGATGGGGCCATGTGGGTGTGCTGATCATAGC
 CTGGTGTGCTGTGTTGGGGCAAGTCACTCGTGTGGGTGTCATCATATACACACAAGCGGAGGAATGAAGA
 TCTGACAGCATTAACACACAGATGAGACCAACTTGGCAGCAGATATCTTAGTTATTTGTCTATCTCAGGGAACGTT
 AGCTGCAGCAGGAGTGGTATGCTGTCTTCAGAAAGTGAAGCCACCAAGTTTGTTCACATCTTCAGTCTCTGG
 ATTTTCTTACCAACATGACAGTAGTGGGACCTGCCATATTGAACAATGACAGTGAAGCTGATGTGGAAGCTGCA
 CACAGATCTTCCCTTTGTCCTGTTTGGGATCCACAGGCCCTATGTAATTTGAAGGGAATGTGATGAGCTCAGA
 TCTTTTGAACATATCATACAGTTTGCAGTCTGACCCAAGAACAGTTTATATGGAACCACTTGAGCCACAGTTA
 CATAAAGAAAGAGTGTCTACAGTTCTCATCTCTCAGAGAAATCTTCGGAACGAGCTTCAATATATATC
 GTGGCCTTCACATGTGAGGAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTCGAATGAAAATCTGTG
 TCTAAACAGTCTCTCTTAGATTATTAGTGCAAATCCAGAGCCAGCGTCCGTTGCTCGAGTAATCTTCTACGGG
 TACCTTTGGAAGAGCTCTCAGGAGACTCACCTAGATGCCATTCAAGCTTTGGACAGCCATCAGATTGTCCAGCC
 AAGAGCTCTTTATTGAAAGCTCATTCTTCCCGAGCTTGGACTTGGGTCAGAGAGATGGGAAGAAAGCA
 AGATTTTCAGGAAGAAATCAGTTTGTACTTTTAAACAGACTTGAAGACTACAGGACTCCAAATTTTCAGTCT
 TTATGATCTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTTAACTACTACCTCAAGTGAACCTTTTATTA
 AAGAGAGAGATCTTTATGTTTTCCTTTAAATGGAGTATGAATTTTAAAGGATATAAAATGCTTTTATATCAGAT
 GAACCAAAATTTACAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAAACTTA
 TTTTTCAGCTTTGTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTAITTTATGATT
 TTATATGCGCAGATTTCTTTTATGAAAATGAGTTACTAAAGCAATTTAAATATACCTCGCTTGTACCAITTT
 TTAATAGAGGTACTCATTAATATTTTGACATTAATATTTAATAAAATGTGTCATATTTGAA

09062652000

FIGURE 102

MVDVLLLFSLCLLFHISRDPDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVPSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLNLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNISAI PPKMFKLPLQLQHLNLRNKIKNVDDLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMELQLDHNNTLETITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLESLDLTFNHLRLDSSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSSKTLTDLKNNE
ISWTIEDMNGAFSGLDKLRLLILQGNRIRISITTKAFTGLDALEHLDSLDAIMSLQGNAFSQ
MKKLQQLHLNLTSSLLCDCQLKWLPOWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSPICSAASSSDSPMTFAWKDNDLLHDAEMENYAHLLRAQG
GEVMEYTTILRLREVEFASGKYQCVISNHFGSSYSVKAKLTVMNLPSPFTKTPMDLTIRAGA
MARLECAAVGHAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIIVDKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSVDSDAGKYTCESNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVIIVAVCCVVGTSLVVWVVIYHTRRRNEDCSITNTDETNPADI PSYLSQQGLAD
RQDGYVSSSGSHHQFVTSAGGFFLPQHDSSGTCIDNSSADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCSDPDPRVTLMMDHYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDPSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFQPSDCQPRAFYILKAHSSPDLDGSEEDGKERTDFQEEHNICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

100170-662066

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAATG
AAGGATGCGAGGACGCAGCTTTCTCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAGAAGGAAGAAC
GAAGCTTTTCTTTGTGAGCCCTGGATCTTTAACACAAATGTGTATATGTGCACACAGGGAGCATTTCAAGAAATGAAA
TAAACCCAGAGTTAGACCCCGCGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
CCACCCCCAAAAAAGGATGATTGGAATTAAGAACCGAGGATTCACAAAGAAAAAAGTATGTTTCATTTTCTC
TATAAAGGAGAAAGTTGACCGAAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTGTTTCTTTCTTTTCTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAGAAAA
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATGTGATTGGGGAGGAAACACGACGAGCACAGTTGGGA
TTTGTGCTCTATGTGTGACTAAAATTGACGGATAATTGACAGTTGGATTTTTCTTATCAACCTTCCTTTTTTAAAT
TTTTATTCCTTTTGGTATCAAGATCATGCGGTTTCTCTGTCTTAAACACCTGGATTTCCATCTGGATGTTGTGCT
GTGATCAGCTTGAATAACACTGTTTGAATTCACAAGGACCAACACAGATAAATTTATGAATTTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGTCTCTAGGTTTAAACAGGCGCCCTATTTGACCCCTGCTGTGTGTGCT
GCTGTGCTCTTCAACTTCTTGTGTGTGGCTGTCTGTGTGCGGGCTCAGACCTGCTCTTGTGTGTCTCTGCAGCAA
CCAGTTGAGCAAGGTGATTTGTGTTTCGAAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACCGCT
GCTGAACCTCCATGAGAACCAATTCAGATCATCAAAGTGACAGCTTCAAGCACTTGAGGCATCTGGAATTCCT
ACAGTTGAGTAGGAACCAATATCAGAACCATTGAAATTTGGGGCTTCAATGGCTGTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAACTCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACTGAAGAGCTCTGGTT
GCGAAACAAACCCCATTTGAAGCATCCCTTCTTATGCTTTTAAACAGAAATTCCTTCTTGTGCGGCACTAGACTTAGG
GGAATTTGAAAAGACTTTCATACATCTCAGAAGGTGCTTTGAAGGCTGTGCTCAACTTGAGGTATTTGAACCTTGC
CATGTGCAACCTTCGGGAATTCCTTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA
TTTATCTGCCATCAGGCTTGGCTCTTTCCAGGGTTTGTATGCACCTTCAAAAACTGTGGATGATACAGTCCCAGAT
TCAAGTGATTGAACGGAATGCTCTTGAACACCTTCAGTCACTAGTGAGATCAACTGGGCACACAATAATCTAAC
ATTA CTGCTCATGACCTCTTCACTCCCTTGCAATCATCTAGAGCGGATACATTTATCATCAACCCCTTGGAACTG
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCTCGAACACAGCTTTGTTGTGCCGGTG
TAACTCTCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACAGAAATTACTTCACTATGCTATGCTCCGGT
GATTGTGGAGCCCTCGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCCGGGCTCCACAT
CCTGACATCTGATCTGTGATTACTCCAAATGGAACAGTCATGACACATGGGGGCTACAAAGTCGGGATAGCTGT
GCTCAGTGTGGTACGTTAAATTTCACAAATGTAACGTGCAAGATACAGGCATGTACACATGTATGGTGTAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCTTGAATGTTACTGACGACCACTACTCTCTTCTTACTTTT
AACCCTCAGAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGACACAGATAACAATGTGGGTCCCCTCC
AGTGTGCACTGGGAGACCACCAATGTGACCACTCTCTCACACCACAGAGCACAGGTCGACAGAGAAAACTT
CACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAATTTGATGAGGTCATGAAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCCATCACCATCATGGCTGCAGTGATGCTGGTCATTTTTCACAAATGAGGAGACGACCA
TCGGCAAAACCATCAGCCCAACAGGAGCTGTTGAAATTTAATGTGGATGATGAGATTGAGGAGACACACC
CTAGCAAGAACCTCAGCCATGCTGCTATCGAGCATGAGCAGCTAAATCATATACTCATATAAAATCTCCCTT
CAACCAACACACAGACTTAACACAAATAAATTCATACACAGTTTCACTGTCATGAGGATGATGATTTATGATCCGAATGAA
CTCTAAAGACAAATACAGAGACTCAAACTCTAAACATTTACAGAGTTTACAAAAACACAAATCAAAAAAAA
GACAGTTTATTAATAATGACCAAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA
AAAAAGAAAAAATTTATTTATTAATAATCTATTGTGATCTAAAGCAGACAAAA

100120-6520660

FIGURE 104

MLNKM TLHPQQIMIGPRFNRLFDPLLVL LALQLLVVAGLVRAQTCPSVCSN QFSKVIC
VRKNLREVDPGISTNTRLLNLHENQIQIIKVN SFKHLRHL EILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRN NPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNL TPLIKLDEL DLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHPWNCNC DIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSN SVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTF TIPVTDINSGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHHTTNTVNTINSIHS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

100170-6520660

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGGCTTCGCGCGCCGGAGTAAAGAAAGGAATTTGACCGGGCAGCGCGAGGAGGAGCGCGCACGCGACCGC
GAGGGCGGGCGTGCACCTCGGCTGGGAAGTTTGTGCCGGGCCCGAGCGCGCGCGCTGGGAGCTTCGGGTAGA
GACCTTAGGCCGCTGCAGCGCGATGAGCGCGCGAGGCTTCCGTGCGCGCGCCGGGGGTGGGGCTGCTGCTGTGCG
CGCGTGTGGGGCGCGTGGCCGGTCCGACAGCGCGGTGCGCGGGAACTCGGGCAGCCCTCTGGGGTAGCCCGC
GAGCGCCCATGCCCACTTACCTGCCGCTGCTCGGGGACCTGTGGACTGCAGTCTGTAAGCTCAACAGATTTATCTTT
CCCGAGCTTCCGCTCTGGGTGCTGCGGTGGACTTAACTCAACAGATTTATCTTTTATCAAGGCAAGTTTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAAGTGAAGAACTGAACAAACATGAATTTGAGAACCATTTCCAAATCTGGGACCA
CTCTCGGCAAAATATTACACTTCTCTCTTGGCTGGAAACAGGATTTGTGAATATCTCCCTGAACATCTCGAAAGAG
TTTCACTGCTTGAATCTTTGAGCTTTAGCACAGCAAAATATTTCAGAGCTCCAACTGCAATTTCCAGCCTTACAG
CTCAAATATTGATTTCTCAACGACAAACGAGTCAACATCAATGGAACTGGGTATTTTGACAAATTTGGCCAAACACA
CTCCTTTGTTTAAAGCTGAACAGGAACGGAATCTCAGCTATCCCAACCAAGATGTTTAACTGCCCACTCGCAACA
CATCTCGAATTGAACCCGAACAGATTAAGAAATGTAGATGGAATGACATTTCCAGGGCTTTGGTGTCTTGAAGTCT
TGAAAAATGCGAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGGAATTTTGG
CAGCTGGACCAATAACACTTAAACAGATTTACCAAGGCTGGCTTTACGGCTTGATGCTCAGCAAACTTATCT
CTCAGCCAAATGCCATCAACAGGATCAGGCCCTGATGCTTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTTCAATCACTTATCAGGTTTAGATGATTTCAAGCTTCTTGGCCTTAAGCTTAACTAAATCAGCTGCACATTTGGG
AACAAACAGATCAGCTACATCTGATTTGCTGCTTCCGGGGGCTTTCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAATTTCTGCGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAACTCAGGCGAGCTGATCAT
CAAGGAATCGATCGCTTCTTATCTAAAGAACCTTCTCTGGTTGGATCGATGGAGCATCTAGACTTGTGAGT
GACAAACCAATCATGTTTCTCAAGGCAATGCAATTTTCAAAATGAAGAACTCGCAACAAATGCAATTTTAAATACA
CTCAAGCTTTTGTGCGATTGCGAGCTTAAATGGCTTCCACAGTGGGTGGCGGAAACAACTTTTCAGAGCTTTTGA
AATGCCAGTTTGTGCCATCTCTCAGCTGCTTAAAGGAAGAAAGCATTTTGTCTGTGGCCAGATGGCTTTTGTGTT
GATGATTTTCCCAACCCAGATGACCGTTTCAGCCAGAAACACAGCTCGGCAATAAGGTTTCCAATTTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTATTTCCCAATGACTTTTGTCTGGAAAAAGACAATGAATCACTGCAATGAT
GCTGAAATGGAAAAATTATGCCACCTCCGGGCCCAAGGTGGCAGGTGATGGAGTATACCAACACTCTTCGGCTG
CGCGAGGTGGAAATTTGCCAGTGAGGGGAAATATCAGTGTGTCATCTCCAATCACTTTGGTTCATCTCTACTCTGTC
AAAGCCAACTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATCTCAACATCCAGATCCGAGGCTGGGGCC
ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCAGATAGCTTGGCAGAAAGATGGGGGCACAGAC
TTCCAGCTGCACGGGAGAGACGATGCAATGTGATGCCGAGGATGACGTGCTTTTATCTGGTGGATGGAAGATA
GAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTTCAGCAATGCAACTCTGACTGTC
CTAGAAAACCATCATTTTTCGGGCCACTGTGGACCGAACTGTAACCAAGGAGAGAAACAGCGCTCCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAACCTGGACCAAGATGATAGCCCATTTGGTGGTAAACCGAGAGGCAC
TTTTTTTCAGCAGGCAATCAGCTTCTGATTTATGTTGGACTCAGATGTCAGTGTGATGCTGGGAAATACACATGTGAG
ATGCTTAAACCCCTTGGCACTGAGAGAGGAAGCTGCGCTCAGTGTGATGCCCACTCCAACCTGCGACTCCCCCT
CAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGATGATGAGCCGTGGTTTCTGT
TGGTGGGCAGTCACTGCTGTGGGTGCTCATATACACACAAGCGGAGGAATGAAGATTCGAGCATTTACC
AACACAGATGAGACCAACTTGGCAGCAGATATTCCTAGTTATTTGTCATCTCAGGGAACGTTAGCTGACAGGCA
CAACATGACAGTATGGGACCTGCCATATTGACAAATGACAGTGAAGCTGATGTGGAAAGCTGCCAGAGCTGTTC
CTTGTCCGTTTTCGGGATCCACAGGCCCTATGATTTTGAAGGAAATGTGATATGGCTCAGATCTTTTGAACACA
TATCATACAGGTTGACGCTGTGACCCAGAACAGTTTAAATGGACCACTTAGCCAGCAATACATAAGAAAGAG
GAGTGTACCCATGTTTCTATCTCTCAGAAAGATCTCGGAACGGAGCTTCAGATTAATATCTGTGGCTTCCACAT
GTGAGGAGCTACTTTAACTAGTTATCTTCAACATGAAGGAGCTGGAATGAAATCTGTGTCTTAAACAGATTC
TCTTTAGATTTTGTGCAAACTCAGAGCCAGCGTGGTGTGCTCGAGTAATCTTTTTCAGGGTACGTTTGGAAAA
GCTCTCAGGAGACTCAGCTTAGATGCTTATTCAGCTTTGGACAGCCATCAGATTTGTCAGGAGGCTTTTAT
TGAAAGCTCATTTCTTCCCAAGCTTGGACTTGGGTGAGGGAAGATGGGAAGAAAGAGCAGATTTTTCAGGAA
GAAATCAGATTTTGTACTTTTAAACGACTTTAGCAAACTACAGGACTCCAAATTTTCACTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGGCTTAAACATACTACCTCAAGTGAATTTTATTTAAAGAGAGAGAAAT
CTTATGTTTAAATGGAGTTATGAATTTTAAAGGATAAAATGCTTATTTATACAGATGAACCAAAATCT
AAAAGATTGAAAGATTTTATCTGGGAATGATGCTCATATAAGAACTTTTAAACATTTTAAATCTTTG
TTTTATGCAAAAGATATCTACGTAAATTAATGATATAAATCATGATTTATTTATGTTTATTTAATGCGGAGA
TTCTTTTATGAAAAATGAGTTACTAAAGCATTTTAAATAACTGCTGCTTGTACCAATTTTAAATAAGAT
ACTTCATTTATTTTTCGACATATATTAAATAAATGTGCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

100120.6520660

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAPERPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSNIT
LLSLAGNRIVEILPEHLKEFQSLLETLDLSSNNISELQTAFPAQLQKLYLYLNSNRVTSMEFGY
FDNLANTLLVLKLNRRNRISAI PPKMFKLQQLHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNTLETITKGWLYGLLMLQELHLSQNAINRISPDWAFEC
QKLSELDLTFNHL SRLDDSSFLGLSLNLT LHI GNNRVSYIADCAFRGLSSSLKTLDLKNNEIS
WTIEDMNGAFSGDLKRLRLILQGNRIRSIITKKAFTGLDALEHLDLSDNAIMSLQGNFASQMK
KLQQLHLNTSSLLCQDLKWLQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF
PKQITVQPETQSAIKGSNLSEFICSAASSSDSPMTFAWKDKNELLHDAEMENYAHRAQGGG
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVMNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHAPQIAWQKDGDTFPAARERRRMHVMPEDDVFFIVDKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPKLNWTKDDSLVVTERHF
FAAGNQLLIIVDSVDSDAGKYTCESMNTLTGERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
TVGVVIIAVVCCVVGTSVLVWVVI IYHTRRRNEDCSITNTDETNLPAIPSYLSSQGT LADRO
DGYVSSSESGSHHQVFTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNYVSGDPFETYHTGCSPPDRTVLMHDHYEPSYIKKKECYPCSHPEESCEFSFNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEEHNHICTFKQTLNRYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

10070-652066

090670-0700

[illegible]

FIGURE 108

MEGEEAEQPAWFHQPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPREENEFAEEEEPVVLVLSPEEPGPGPAAVSCPRDCACSQEGVDCGGIDLREFPGDLP
EHTNHLSSLQNNQLEKIYPEELSRLETLNLQNNRLTSRGLPEKA FEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFGSSNV
EVLILSSNFLRHVPKHLPPALYKHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSV DANVLTPIRSLEYLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISK
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

100170-6522560

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGGCTCGCCGCTGTCTCCGGGAGCGGCAG
CAGTAGCTCCGGGCGCGCAGGGCTGGGGGTTCTTCGAGACTCTCAGAGGGGGCGCTCCCATCGGCGCCACACACC
CAACCTGTCTTCGCGCGCCACTGCGCTGCGGCCCAGGACC CGCTGCCCAACATGGATTTCCTCTGGCGCTGGT
GCTGGTATCTCTCGCTCTACCTCGAGGCGGCGCCGCGAGTTTCGACGGGAGGTGGCCAGGCAAAAGTAGTGTATCGAT
TGGCCATATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTGACCC
TGTGTGCCAACACAGATGCCAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCATCTGGTATTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGTGAAGCACAGGTGTATGAACACTTA
CGGCAGCTACAAGTGCTATGCTCTCAACGGATATATGCTCATGCGGATGGTTCCTGCTCAAGTGCCCTGACCTG
CTCCTATGGCAAACTGTAGTATGGCTGTGATGTTGTAAAGGACAAATACGGTGCCAGTGCCCATCCCTGGCCCT
GCACCTGGCTCTGATGGGAGGACCTGTGTAGATGTGTATGAATGTGCTACAGGAAGAGCCCTCTGCTGCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCAATAAGGCTTGATCTCATGTATATTTGGAGG
CAAATATCAATGTATGACATAGACGAATGCTCAGTTGGTCAGTATCAGTGCGACGAGCTTTGCTCGATGTTATAA
CGTACGTGGGTCTTACAGTGCAGAAATGTAAGGAAGGATACAGGGGTGATGGACTGACTTGTGTGTATATCCCAAA
AGTTATGATTGAACCTTCAGGTCCTCAATTCATGTACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGGGAAGTACTTGGTGGCCCTCCGAAGACACCATATATTCCTCTATCATTACCCAA
CAGGCCACTCTCTAAGCCACACAAAGACCTACACCAAAGCCACACCAATTCCTACTCCACACCAACCCACCC
CTGCCAACAGAGCTCAGAACACCTCTACACCTACAACCCAGAAAGGCCAACACCCGGACTGACAACTATAGC
ACCGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGACCTCAGAAACCCAGAGG
AGATGTGTTCAAGTGTCTGGTACACAGTTGTAATTTTGACACTGGACTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCCTGGGAACCAATCAGGGACCCAGCAGGTGGACAAATCTGACAGTGTGCGGACCAAGGCCCAGG
GGGAAAAGCTGCACGCTTGGTGTCACTCTCGGCCCGCTCATGCATTGAGGGGACCTGTGCTGCTCATTCAGGCA
CAAGGTGACGGGGCTGCACTCTGGGCACACTCCAGGTGTTTGTGAGAAAAACCGCTGCCACCGAGGACGCTGTG
GGGAAGAAATGTTGGCCATGGCTGGAGGCAACACAGATCACTTGCAGGGGGCTGACATCAAGAGCGAATCA
AAGATGATTAAGGGTTGGAAAAAAGATCTATGATGGAAAAATTAAGGAACCTGGGATTATTGAGCCTGGGAAG
AGAAGACTGAGGGGCAACCAATGATGGTTTTCAAGTATATGAAGGGTTGGCAGAGAGGGTGGCGACAGCTG
TCTCCATATGCACATAAGAAATAGAACAGAGGAACTGGCTTAGACTAGAGTAAAGGGAGCAATTTCTTGGCAGG
GGCCATGTGTAGAATACCTCATAAAAAAAGAAAGTGAAGAAATCTCAGTATCTCTCTCTTTCTAAAAAATTAGA
TAAAAATTTGCTATTTAAGATGGTTAAAGATGTTCTTACCCAGGAAAAGTAAACAAATTATAGAAATTTCCCAAA
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAGAAATCTTTAGAACATAAATAATTTGGACAAGGCTTAATTTAGG
CAATTCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCACCAAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCTCAGCAGTATTAAGAAAAAAGGAACTATTTATTTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTCAATGTTTCTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGAGTGTTCAGATTTTTTTTTTTTAAAGAGATCCTTCAAGGAAACAGATTCAGAGAG
ATTTTCATCGGGTGCAATCTCTCTGCTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGGCCCTGGCCC
ACACCGGACAGACTTTCTTCCCTCACCCTATCAGTATGATTCAGTTTCTCTTATCAATTTGAGCTCTCCAGGTTCCAC
AGAAGAGTAATATTTTGTGAACAAATAGGTACAAATGAAGGCTTCTGCTCAATTTAACCTGCTAAAGGACAGTGGG
AGGGGGAATAATAATCTTAAGCCTTGGAGTAAACGCGAAGATATATGGCTAGATCATTTTAAATGGTTCAAT
TCCTTTATTTAGTATCAATACTGCACAGCTGAAGATGAAAGGGGAAAAATGAAGTAAATTTTACTTTTCTGTCGCA
TGATACATTTGCACATAACTGATGGAAGAGTTATCCAAAGTACTGTATAACATCTTGTTTATTTTAAATGTTT
CTAAAAATAAAAAATGTAGTGGTTTTCCAAATGGCCTAATAAAAACAATATTTGTAATAAAAAACACTGTTAGTAAT

09902759-071004

FIGURE 110

MDFLLALVLVSSLYLQAAAEEFDGRWRPQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIIPKVMIEPSGPIHVPKNGTILKGD TGNNNWI PDVGSTWWPPKTPYIPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTD P Q K P R G D V F S V L V H S C N F D H G L C G W I R E K D N D L H W E P I R D P A G G Q Y L T V S A A K A P G G
K A A R L V L P L G R L M H S G D L C L S F R H K V T G L H S G T L Q V F V R K H G A H G A A L W G R N G G H G W R Q T Q I
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

09905759 - 07001100720

CTCTCTTTGAAAAGGATATATCACCTGATCAGGCTCTCTCTGCATTTGCCCTTAGATTGTGA
AATCTGGCTCAAGGCTCTTACAACCTTTCTTCTCTGCTTTGCAACAGAGTGCTTGCTCGGGCTGTA
 AGGTGACAGTGCATCACACATGTCCATGGCTGCAGAGTGAGCCCTCTACCTACCGCTG
 CACTATTGGCTTCCACACTCCAGCATCAGACATCAGATCATATGGCTATTATTGAGAGACCCCA
 CACAATGGCCAAATACTTACTTGGGCTCTGTGAATAAGTCTTGTTCTTGACTTGGAAATACC
 AACACAAGTTTCCACATGATGCCA CCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCC
 GATGAAGGCAATTA CTCTGTGAAGGTCAACATTACGGGAAGATGGAATCTTATCTGCGCATGA
 GAAGATACAAGTACCGTTGATGATCTCTGTCACAAGCCAGTGGTGCGAGATTCACTCTCCCT
 CTGGGGCTGTGGAGTATGTGGGGAACATGCCCTGACATGCCATGTGGAAGGGGGCACTCGG
 CTAGCTTACCAATTGGCTAAAAAATGGGAGAGTCTCCACACAGCTCCACCTACTCTCTTTTC
 TCCCCAAAAAATACCTTTATATTGGCTCAGTAACCAAGGAAGACTTGGGAATACAGCT
 CGCTGGTGAGGAACCTTGTCTCAGTGAATGAAAGTGATATCAATTATGCCCATCATATATTAT
 GGACCTTAGGACTTCAAGTGAATCTGTAAAGGGCTAAAAAGTAGGGGAAGTGTTACTGT
 TGACCTTGGAGAGGCCATCTCTATTGATTGTTCTGTCTGATTCTCATCCCCCAACACTTACT
 CTCTGATTAGGAGGACTGACAATATCTACATATATCATTAAGCATGGGCTCGCTTGAAGTT
 GCATCTGAGAAAGTAGGCCAGAAGACAATGGACATATGTGTGCTGTGCTTACAACAACATAAC
 CGGCAGGCCAAGATGAAACTCATTTACAGTTATCATCTTCCGTAGGACTGGAGAAGCTTG
 CACAGAAGGAAAAATCATTTGTCACTTTTAGCAAGTATAACTGGAATACTACTATTTTGATT
 ATATCCATGTGTCTTCTTCTATGTGAAAAAAATATCAACCTCAAAAGTTATAAAACAGAA
 ACTAGAAGCGACGCCAGAAAACAGAAATCAGGAAGCTCAAAACTTTTCAGGCCATGAAGATG
 CTCTGGATGAGTTCTCGAATATATGAATTTGTGCTTTTCCAGATGTTTCTGGTGTCTCCAGG
 ATTTCAAGCAGGCTCTGTTCCAGCCTCTGATTGTGTATCGGGCAAGATTTGCACAGTACAGT
 GTATGAAGTTATTTCAGACATCTCCCTGCCAGCAGCAAGCACTTCCAGAGT**GAA**CTTCTATGG
 CTAAAAAGTACATTCGATGAAATTTCTGAAGAAACCTTTTAAGGAAAAAACAGTGGAAGAT
 ATATTAACTTGGAAATCAGTGAAGAAACAGGACCAACACCTTTACTCATATTATCTTTTACA
 TGAGAAATAGAGGCATTATGCGAAATGAATGCAGGTTTTCAGCATATACACAATGTCTT
 GTGCAACAGAAAAACATGTGGGGAATATTTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
 GGAGAAGCAAAAGTGACAGGGGTTTCTCTAAGTTTGTATGAAATATTCTCTACAAACCTCA
 ATTAGTTCTTACTCTACACTTTCACTATCATCAACTGAGACTATCTGTCTACCTTACCTAA
 TGTGGAAACTTTACATTTGTTTCGATTTTTCAGCAGACTTGTGTTTATAAATTTTATTAAGTG
 TTAAGAATGCTAAATTTATGTTTCAATTTTATTTTCCAATTTCTATCTTGTTATTGTGACAA
 CAAAGTAATAAGGATGTTGTCAAAAAACAAACTATGCCCTTCTCTTTTTTTCAATCACC
 AGTAGATTTTTTTGAAGAGACTTGTGAACACTTAAGGAAGATCATTTAAAGCTCTTATTTT
 TTTTTTTCAAGGAAGATGAGTTCAATAAATATTTCTGTTTTGCTTTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVGRQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMEDIIIMPIIYYGPYGLQVNSDKGLKVGVEFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

100120.6526660

FIGURE 113

GCAAGCGGCGGAAATGCGGCCCTCCGGGAGTCTTGCA GTTCCCTTGGCAGTCCCTGGTGTGTT
GCTTTGGGGTGCTCCCTGGAGCGCACGGGCGGCGGAGCAACGTTCCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGGCCCTGTCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGTCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCAAGAGCAGCCAGGACTGAGTGGACGGTTTATCATTAACGTCTC
TTCCCTACTATTTATCATTGTAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGATTGAGCCGCTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAAGCTCTTTGAGTATCTATGTGGA
TCAGGACGTGCCATAACTTTTATGAAGACCTTGATTGCGAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCCTTGTCTTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAAAACAGAAGATTGATCATTTTGTTGGTTTGAAGTG
AATCTGTA CTTTTTGAATATTGCAAGGTTTCACTGATATTGTCATTAATTAAGAGAGTCTA
CATTGAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTAAATAGTTCCTAATTTTGA AAAATCGTGCCAAGCAATAAGATTATGTATATTTTGT
TTAATAATAACCTATTTCAAGCTGAGTTTGA AAAATTACATTTCCCAAGTATTGCAATTAT
TGAGGTATTTAAGAAGATTA TTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTCACTGACAATTTCTGTGTTTCTTACTTACTATGGGTTACATTTTATTTT
AATTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTCAGTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAAGTTTCACTGATTTCTCTTGATTC
CAACAAAGTTTGATTTTCTCTGTATTTTCTTACTTACTATGGGTTACATTTTATTTT
CAAATGGATGATAATTTCTTGGAACATTTTATGTTTTAGTAAACAGTATTTTTTTGTT
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATGAACAATCTGTTGTAATTTAAAAAT
TTGGCCACTTTTTTCAGATTTACATCATTTCTGCTGAACCTTCAACTTGAATTTGTTTTTT
TTTCTTTTGGATGTGAAGGTGAACATTTCTGATTTTGTCTGATGTGAAAAAGCCTTGGA
TTTTACATTTTGA AATTTCAAAGAAGCTTAATATAAAAGTTTGCACTTCTACTCAGGAAAAAG
CATCTTCTGTATATGCTTAAATGTATTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTTAA AATAATAACATTTTATATTTTAAAAAGACAA
ACTTCATATATCTCTGTGTTCTTCTGACTGGTAATATTGTGTGGGATTTACAGGTA AAA
GTCAGTAGGATGGAACATTTTGTGTATTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAGAGAGGGGAAAAATCATAATACAAATGAATCAACTGACCATACGTAGTAGAC
AATTTCTGTAATGTCCTCTTCTTAGGCTCTGTTGCTGTGTAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTTGTACCATT
AAAGATTTGGAATGTGTAACTTGTGATGCCTTAGAAAAATATCCTAAGCACAAAAATAACCT
TTCTAACCACTTCATTAAAGCTGAAAAA AAAAAAAAAA

09902759.071001

FIGURE 114

MAPSGSLAVPLAVLVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKKLLSESAQPLKKVEEEQEAEDEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

100120-6522050

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCAATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGAGGCGGAATTCCTCACCTCTATTG
GGCACAATGACTGACCTGATTTATGACAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGTCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGGCTAAACACAGACTGGCCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTTATCGCCAACTCTCTGTGCAGCGGCAGTTCTTCCCACTGATGAGGACGAGTAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
GAGGGGAACTTCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
GGCCGCTCGGCTTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTACAGGTGCTGACTACCTCA
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTC
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAAACAAATCAGACAGAACTGAGCTAGCAACCCAGAGGCA
TCTATGAGAGGCCGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTGG
GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
CAGGGCCCCACAGCTGCTCATTTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCCGCACA
TCGTGAGGTACTACGATGTCTGCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGACAGCCACCGTTCGTGATCCCAAGACAGGAGTCTTCACTGTGCGCAGCTA
CCGGGTTTCCAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCCAGTAAATC
GTCGGATGCAATATCACAGGTTAAACAGTAAGACTGCAGAAATGTTTACAGTTTGCAAAAT
TATGAGTGGGAGACAGTATGAACCGCACTTCGACTTCTTAGGCGACCTTTTGACAGCGG
CCTCAAACAGAGGGGAATAGGTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGGCGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCTGCC
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGATTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTCTGTCTTCCCTTCTCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTCTTATCAGGCT
GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCAGCCCTTCCATTGAGCTGTGCCATCCTTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTTCACTGAACCAAGTTCTGATACCTTGTGTTACATGTTTGTGTTTTAT
GGCATTCTCTATCTATTGTGGCTTTACCAAAAAATAAATGTCCCTACCAGAAAAA

100120-6522060

FIGURE 116

MKLWVSALLMAWFGVLSVCVQAEFFTSIGHMTDLIYA EKELVQSLKEYIILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPAL ELDVLQDSAAGFIANLSVQRQFFP
TDEDEIGA AKALMRLQD TYRLDPGTISR GELPGTKYQAMLSVDDCFGMGRSAYNEG DYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLR
YFEQLLEEEEREKLTLTNQTEAELATPEGIYERPV DYLPERDVYESLCRGEKVKLTPRRQKR LF
CRYHHGNRAPOLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYSMDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGE GDYR
TRHAACPVLVGCKWVSNKWPFHERGQEFLRPGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

090259-0101

CCAGTATTAGGTTTACTCTTCTCTTCTTTTGTAGTGAAGACAGCAATAATCCGAGTGTGAGTAATGTATTGT
TCTTATTATACCGTTTGGCTGCGGGGTAGTTTCCGACACCTTCCAGATTGAAGACAGCAGGAGGATGTGGA
AGACAGACCAATCTTCTTGGGATGCTGGTCTCTGGAAGTCCAGCGGGCTTGCTCTGTTTCTGGCCCTATGACC
CAGGTTTCTGCTTTAAACTGAAGGCCCTACTCTGGCTGCGTGGCCATCAATCATGATCTTGTAGGCTGTGCC
CCTGGGGACCCCACTGGCAGGGCCTACCAACATGCGACTGAGCTCCCTGTTGGCTCTGCTCGGCACGGCCTC
CCCTCATCTTAGGGGCTGTCTCTGGGGTGCAGCTCTGAGCCCTCTCGCGGTTCTCTGGATCTCGGGGGAGGAGAG
ATCCCTGTGTGGAGCTGTAGGGAGCAGGAGGGGCGACAGAACTCAGATTCCAGAGCTCGGGCTAGACCAAAGT
ATGAGACTCTCAAACCCGGATGTGCCCTATCAAGGGAACCCCAACAGCCCTACAAGAAAGGTCTCGAGGACT
GGTACATCCAGCAGAGCTGGGCTCCGTGAGCGAGTGTCGTGGTGCTGTCTGACTCTCCGGGTACTACATGTCCA
CTTGTGGCGTGGCTGTGAACCTGACGTGGGCGGCATCTCCCTGGTGTACTTACTCTTAGCTGGGCACGGGGGG
CCGGGCTCTGACAGGAGTGCAGTGGTGTCTCATGGGATGAGCGGCGCTGGCTCATGTGACAGACCGGGG
GCACCTCTCACACACCTTTGGGGCGCACTAGACTGTTCTTCATCACTGACAGATGACATCATTTGTGACGGCC
CCCGCTGGCAGCCCTTGTCTGGCACTCTCAGCATCAACACAGACTGTACTTAGGCGGGGACAGAGATCTCAITG
TGGGGCGGACGAGCGCCGGTATCTCATGGGGCTTTGGTCACTGTGTTGCACGAGTCTCTGCTTCTGCTGTGC
GGCCACATCTGGATGGCTGCGAGGAGACATCTCAGTGGCCGCTCTGACAGTGGCTTGGACGCTGGCCCAITG
ACTCTTGGGGCTCGGCTGTGTTCTACAGCACAGGGGACGAGTATGCTCATTTGAATCTGGACAAATATAGG
ACCTTGAGAAAGAGGAGCTCGGCTTCTCAGTGGCTCTCGCCCTGCCCTGTCTCGAAGGTACCCCTAGT
ACGGCTCCCAACAACCTCTCAGCGCTCTGGAATGTGGAGCGGGCTTACGTTGAATAGAAACACTCAGGCTCAGA
TCCGGAATCTGACCGTCTGACCCCGAAGGGGAGCAGGCTGAGTGGCCCTTGGGCTCCCTGCTCTTCTT
TACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCAACAGACGACACACTCTCTCTGTCAGATGGGG
CTCCAGTGGCCCACTAGAGGGGCTGACGGGGCGAGCTGGGTGATCGTTTGGAGATGCCCTGGAGACGTCA
ATCGGCGCTTACAGCCCCCTCGGCTTCCAGAAAGCAGCATCTCAACGGCTCTCGGCGCTTGGACCTGCA
GGGACATGGAGTACGCTGCTGACCTGCTGTTTGGAAATGTGACACAGCGTGGGACCGGGCGGCTGGCTGCA
GGTCTAGCCTGCTCGGGCACTGAGCCGGGTGGAAATCTACTATCGCTTATGTCACTGAGGCCACCGGAGTGC
AGCTGGTGTGCTGCACTCTGGTGCTGAAGCTGCTGACGCGCCGCTTCTCTCAGAGGTTTGGACGCAATGTG
TGGAGCCACGAGAACTGCAATCTGCTCACTCTGTTCTGTGCTGACGGGCAAGAGAGTGGCGTGGAGCTCAG
ACCCATTCTTCTGGGTTGAAGCTCGACGACGGATGTAGAGCGACGGTACCGCTGGGACAGGCTGGCTGCTGCT
CTGTGCGAGCAGAGGCCCTCTCCAGAGTGCAGTATGAGCAGTGTCTCGAAGAGACCTCTGGTGGACATCTCT
TCTTCTCTACACCGTGTGAACAGGCGTGGCCCGAAGTCTCAACCGCTGTGCAATGATGACCTCTGTGCT
GGCAGGCTCTTCTCAGTCTGTTTCCAGAGTTTCAATCTGCCCTGTACACAGAGATCACCCNAGGGCCCC
CGGGGCTGTGCCCTTGACCCCCCTCCCCCTCTGGTGTGTAACCTCCGGGGGGCTCTATAGGGGGAGGATTTG
ACCGGACAGGTTTCTCGGAGGGGCTGTTCTTCAACAGCTGACACTCTGGCGGCGGAGCGCGCTGGAGTGAAC
TGGCAGTGGCGAAGAGAGGAGAACCTCTGGAGGGCTGGAGGTGATGATTTTCTCTCGGTTCTCAGGCTCTG
ACCTCTTCTCGGGCTGAGACGAGGCGTGGTGACAGATTTCTCCTTGGAGATCGAGGCCACGGCTCAGTGAAG
AATCTTACCACCGCTCGGCTGCTCAGACTCTGGAGGGCTGAGGGGCGTGGCCAGCTGCTGATGCTCTCTT
AGCAGGACGAGGCGCAATGACATCTAGCGGCGCTGGGGGCCCTAACTCATTACTTTCTTTGTCTGCCGAGCG
CCAGGAGGGGACGGCAAGATGGTGGACAGATAGAAATTTGTGCTGATTTTTAAATATGAAATGTATTAA
ACATGTTCTTGCC

0902750-01001

MRLLSLLALLLRPALPDLGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPDSSRARLD
QSDDEFKPRIPYVRRPNPKYKVKVLRITQTELGSRERLLVAVLTSRATLSLTAVANRTV
AHHFFRLLYFTGQRGARAPAGMQVSHGDERPAWLMSERTLRLHLHTFGADYDWFIMQDDTY
VQAPRLAALAGHLSINDLYLGRAEFBIGAQEYQYRCHGGFYLLSRSLRLRLPHLDGCRG
DILSARPEDWLGRCLSDLGVGCVSHQOQYRSEFLAKNRDPEKEGSSAPLSAFAPVHPSE
GTLMYRLHKRFSALELERAYSEIEQLQAIRNLTVLTPGEAGLSWVPVGLPAPFTPHSRFEV
LGDVFTQETHTFSCADGAPKCPQLQASRADVGDALETALETQLNRRYQPRLRFQKQLRLNGYR
RFDAPMEYETLDDLLECBQTPQRHRRALAKRVLSLRLSRVLELPMFYVETATRVLPDLPL
VAEEAAAAPALEAFANVLEPREHALLTLLLVYGPREGGRGAPDFLGVKAAABALEGRYYPG
TRLAWLAVRAEAPSQVRLMDVYVSKKHPVDTLFFLTITVTPRGPEVLNRCRMAISGWQAPP
VHFQEFNPALSPQRSPPGPPGAGDPDPSPGADSRGAPIGRFRDQASABGCYNADYLAA
RARLAGELAGQEEEEELEGLEVMDFLFRPSGLHLFRAVEPGLVQKFSRLDCSPRLSEELYHR
CRLNSELGLGGAQALAMALEQEONST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

0695050

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAATAGAA
TGCACCACCATTGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACGTATTATCCTTGTAANAACC
CAAAGATGTGAGTCTTTGGGGTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCTTGACGCGCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACATATAAAATCTGGAGACCTTGAATAT
TGGGGTATGGAAGGAGGAATGTCTTAAGTGTAGAAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAAGAAAGTGTCTCTGAACAGGGAGGAGATTTTGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAGATATGGCTGTTACTTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTAACTCCAATGGTTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACACATATCCA
TACAGCTGTATGTTCTTTTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTTAAACACATGAACATTGTAATG
TGTTGGAAAGAAGTGTTTAAGAATAATAATTTTGCAAAATAAATATTAATAAATATTATAT
GTGATAAATTCTAAATATGAACATTAGAAAATCTGTGGGGCACATATTTTGGCTGATTGGTT
AAAAAATTTTAACAGGCTCTTAGCGTTCTAAGATATGCAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACTTTTAGCTGTGTGTTCCCTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTTCCAATGGATTGTCCTTCTCAAATGTACAACCTAAGCACTAAAGAAA
ATTAAGTGAAGGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCFEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFN
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGLHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

100720.65220660

100-443887-100

[illegible]

FIGURE 122

MNSSKSSETQCTERGCFSQMFLLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCPLNWEYFQSSCYFFSTDITISWALSCLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTSLSFWDVGEPNNIATLEDCAIMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

100720-652066

069278-2

GGGACATCAAGCGCGCGCGCGCTGCGCGTGGCCCCAGCAACCTCGACATGGCGCGTGAGCGCGGCCACCGCGGAC
TCGGCGCTTCGCGCTCGGCTGCTGCATCTTCTTCGTGCTGCTTTTCAGGGCGCTCGCTGATAGGGGCTGTAAATCT
TCAATTCAAGCATCAAGAACCCCACTGGTATGACAGGAATTTGAAAGTGTGGAAGCATGTCTTGTCATCATTCAGGATTCGC
AGACATGACATGCCCAAGGATTCAGATGTCAGGAGAAATTCAGATATGAACAACCACTATGTGTGTTTTTGACAAACAAA
TTCAGGAGCATTTGGCGGCTGCTGCAGAAATCATGGCGGAAGCATCTCCAGATATCGGAATGTGACACGGAGAG
ACTTCAGCCCTTTATTCGCTGTAGGTGCTGTTGCTCGAAATCGACCGCAGGAAGATTTGATGAGATTTGATCGACAGTTAA
CTGCTCAAGTGAAGCAGTGCAGCCCTGCTCTGTAGATGTCGGAAGGCTGTACAGTATGAGCGAGATGTGGCAATCTGC
ACTGCTCAGGAGATGAGGGGACACCCCGGCTTCATCAGCTGGTATTCGATATGCAATCATGTACCATCTGCCACGGATT
CCAGAGCAATTCAGAGATTTTGCRAATTTCTTTTCCATCATTCGAAAGAGGCATTTTGGTGTTCAGTCGT
TTCACAAAGCAGCATCTGGGACGATCTACTGCTGATTGCTTCCATACGCGAGGCTCAGGACGGGTGTGAGGAGCAGC
AGATGGAGGTCTATGACCTGAACTATGGCGGAATTTATGGGGGGTTCGTGTCTGCTGTGATCTGGCCCTGA
TCACGTTTGGGCATCTGCTGTGATCATCAGACGTGGCTACTTCATCAACATAAAGCAGGATGGAGAAAGATTCACAGA
ACCCGGGAACACAGATGTAGTTTAACTACATCTGCAGTCAGGAGGGGCGATTCAGACACAGTATCGTGTG
TGATCTGACACCCCGGTGTGGCTGTGAGAGCGCACAGGCGCAGCTGCATACCTCTGCTAGAAATCTCTGTGCAA
GCGCAGCAGAGCTGATGCTCGACAGAGCTAGACATCATTCAGAGCTTTTCGTTTGGCTCGCAAGGTGTGACCA
CTACTCTCTTATCTTCAACAGGACATGAAATAGAAATTTTCTCAGATAGCCGCGGTAATAATACCAACA
GGAAGCGAAATCGGTCGGTCTCATGATGTGGGTTCTTAATCTGTTTGTGGCTGATTCGCGATGAGTATAGG
GTGATCTTAAAGAGTTTTCCTCAGCTAAACCGCGCTGTGGCCCTGTGGAAGCAGCATCTTCACAGTGTGCTGTT
CAGCAGCAACCGACAGCAGCATGTGAGATGGCGAGGTGCTGAGACAGCAGCAGCGCATCTCCGCGGGGAACCCA
GAAAAGGCTTTCTTACACAGACGCTTTGATGATCTGCTGACACAGCAGCAACCAACCGATTTCTCTTAAAGGCTCTGC
TGATCGGTTGTGAGCTGTGCATTGTGAGAGAGCTTTTGGATCAGCAATTTGTAAACAACCAAAATCAGGAAG
GTAAATTTGCTGTGAGAGAGGGATCTGCTGCTAGGAACCTCTGCTGTCCAACAGGGGTGTCAGGATTTAAGGAA
ACCTCTGCTTAGCTTAGGCTATGCTGAAATGGTATTCGTAAGTAAATGCTTTCTTAAAGTAAATATATATTTG
CATCATCTAAATTTTCTAGAGATGTATTTTGTATTTAGAAAGAAATTTCTATTTAAACTGTAAATATATTTG
CATACATAGTTAAATTAACCTATTTTTTAAAGAAATCTCAACTGTAGAGATTTTCAAGTCTATGTGTAAAT
TGGAAATATCAATAATTAGAGTATTTTACCAAGAAATCTCTCATCTGAGAGTTTACGTGATGTTCCTTTCT
CATCAGAGTTTGGCTCTTTTACAGAGGAATCATATCTGTCTACATCATCAGACATAGTTCGTAGGAATCTT
TAAAAATTCGATTAAGCAATGTGAAATCAGTTTCTGCTTTCAAAGAAACCTCTCAGTGTAGCTTTGAACT
CGCTCTCTCTAGATATCAGGAGACGTCTGACCCAGGACCCAGGAGCTTCAGATGTACATCAGATG
CCGCTCAGCTCTCGGGTGTGCGCAGGCGCCCGGCTCTAGCTCATGTGTGCTTCGCTGTCTCCGAGGAGCCCT
GCCATCTTGGGCGCTGGCAGTGGCTGTGTGCCAGTGAGCTTTACTCATCGTGCCCTCTGCTTCCAGCAGCAGC
TTCAGGTGGGCACTCAGGAGACATGTGTGTTCTCATGTAGCTCCGAGCTTTTGGGCTGTGTAACAGACCTCT
TTTTGGTATGATGATGGCTCAAAATTAAGGCGCCCAATGCTATTTTTTTTTTTTAAAGTGTTAATTTATTG
AAGATGTGTCAAGGCAAAAGCAATTCGAAATCAAGTCTGCPAAGTACAATAAGCATTTTAAAGAAACATGTGAT
CCCACTGTCTCTCTTGTCCACAGAGAAGACCCAGCAGCCACAGGCTGTGCTGCATTTCAAACAACCAATGAT
GGAGTGGCGGCGAGTCAGCGCTTTTAAAGAAAGCTCAGGTGGAGCAGCAGGTGAAAGGCTGCGGSGAGGAAAG
TGAACACGCTGAAATCAAAGCATTTTCTTAATTTGACTTTTAAATTTTATCTCGCGCGGAGACATGCTCCCAT
TGTGGGGGACATTAGCAATCATCCTACAGAGGCTGTGTTCTCAAGAGCAGGTGTCTCAGGCTCAGCTGCCCT
CGCGTGTGCTGATCAGGATGAAGTGTCTGTAAGCAGAGAGCTGTGAGAAGGAGCATCCACTGTGTGCTGTGGA
GATGTGCTCTACTACTCACCTGTGCTTCTCAGTCTCCAGTCTGTGGGTTTTTTATCTTTAGACGTTTTTTT
AATTGTCATACATAGAGATGTGTTGACTTTTTTTAGTATTTGAAACATCTTGGCCAGCGGCTCTGGACAGGCA
GGAATGGCTCAGCAGTGGCTCAGTGGCTCCTGTGCTGTGCTGATGGCATCTGGATGTCTAGATCAAGTGT
CTCTCATCTGTCACCTCTTGTGTAGAGAGGATGGCTCCCCCCTCAGGTTGGGGATTCAGGCTCAGGCTGCT
TCTTGTGTGTACATGTGATAGGTAGTCTTGTGCCCCCTCTCTTATACCTTAAACCTTCTACACTGTAGTCCA
TGGGACAGCAGGTCTGAAAGAGTAGAGAGAGTGAAGTGAAGTGTGGAAGATGCTGCTTAAAGTGTAGATAGA
CGGAAAGGAATACTCTGTGTTATTTTAAAGATGAATGTGAGCTCAGAGCTCAGGCGGACATGAGGCTGTGATCT
GCTTTTGGATGTGCTGTGCTGTACAGATGCTACAGACTGTGATCTAACACACCGTAATTTGGCATTTTGTAACT
CTATTTTTAAAGGCTCTCAAAGAACCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQQDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGLTVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIIGGIIGG
VLVVLAVLALITLGICAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

09902759-071001